

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 26, 2006, 12:29:46 ; Search time 74 Seconds  
(without alignments)  
362.191 Million cell updates/sec

Title: US-09-980-672-2

Perfect score: 342  
Sequence: 1 SHLVKCAKEKTEFCVNGSEC.....GDRCONVMASTFYAEELVQ 61

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqe, 439378781 residues

Total number of hits satisfying chosen parameters: 1199344

Minimum DB seq length: 0  
Maximum DB seq length: 61

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*

- 1: Geneseqp19808:\*
- 2: Geneseqp19908:\*
- 3: Geneseqp20008:\*
- 4: Geneseqp20018:\*
- 5: Geneseqp20028:\*
- 6: Geneseqp20038:\*
- 7: Geneseqp20048:\*
- 8: Geneseqp20058:\*
- 9: Geneseqp20068:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	342	100.0	61	8	ADE45192 Human neu
2	342	100.0	61	8	ADFO9196 Human neu
3	342	100.0	61	8	ADF32008 Recombina
4	342	100.0	61	8	ADM28541 Human neu
5	337	98.5	60	2	AAR55660 EGRF3. 3/
6	337	98.5	60	2	AAR46919 EGRF3. 3/
7	337	98.5	60	2	AAR67251 Human epi
8	337	98.5	60	2	AAR96077 Epidermal
9	337	98.5	60	2	AAW09364 EGF3. 8/
10	337	98.5	60	2	AAR87462 Epidermal
11	316	92.4	58	3	AAB12601 Human neu
12	307	89.8	57	9	ADY28292 Novel Erb
13	300	87.7	53	6	AAB36804 Human neu
14	300	87.7	56	9	ADY28279 Novel Erb
15	298	87.1	56	3	AAB36802 Protein #
16	294	86.0	52	2	AAW05183 Neu diffe
17	294	86.0	52	3	AAB36792 EGF-like
18	294	86.0	53	8	ADN48886 Human her
19	293	85.7	56	3	AAB36801 Protein #
20	287	83.9	50	2	AAR87457 GGF2bpb5
21	287	83.9	56	3	AAB36811 Protein #
22	282	82.5	56	3	AAB36796 Protein #
23	279	81.6	56	3	AAB36808 Protein #
24	276	80.7	56	3	AAB36799 Protein #

25	276	80.7	56	3	AAB36797 Protein #
26	274	80.1	49	5	AAG66044 Rat NRG-1
27	274	80.1	52	3	AAB36728 EGF-like
28	272	79.5	56	3	AAB36804 Protein #
29	272	79.5	56	3	AAB36795 Protein #
30	271	79.2	56	3	AAB36800 Protein #
31	270	78.9	56	3	AAB36798 Protein #
32	269	78.7	56	3	AAB36794 Protein #
33	268.5	78.5	49	3	AAB36714 EGF-like
34	267	78.1	56	3	AAB36805 Protein #
35	266	77.8	52	3	AAB36725 EGF-like
36	264.5	77.3	49	3	AAB36716 EGF-like
37	263	76.9	52	2	AAW05182 Neu diffe
38	263	76.9	52	3	AAV69983 NDF/heres
39	263	76.9	52	3	AAB12602 Human NDF
40	263	76.9	56	3	AAB36812 Protein #
41	260	76.0	52	2	AAW05185 Neu diffe
42	260	76.0	56	3	AAB36809 Protein #
43	256	74.9	56	3	AAB36810 Protein #
44	254	74.3	52	3	AAB36722 EGF-like
45	252	73.7	56	3	AAB36806 Protein #

# ALIGNMENTS

RESULT 1  
ADE45192  
ID ADE45192 standard; protein; 61 AA.  
XX  
AC ADE45192;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Human neuregulin protein SEQ ID NO:4.  
XX  
KW neuregulin; viral myocarditis; cardiomyopathy; myocardial infarction;  
KW cardiac; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003099300-A1.  
XX  
PD 04-DEC-2003.  
XX  
PF 15-MAY-2003; 2003WO-CN000355.  
XX  
PR 24-MAY-2002; 2002WO-CN000349.  
XX  
PA (ZENS-) ZENSUN SHANGHAI SCI TECH LTD.  
XX  
PI Zhou M;  
XX  
WP: 2004-042705/04.  
XX  
DR N-PSDB; ADE45191.  
XX  
PT New composition comprising neuregulin (NRG), nucleic acid encoding NRG or  
PT an agent that enhances the production and/or function of NRG, and a  
PT therapeutic agent, useful for treating or preventing heart diseases, e.g.  
PT viral myocarditis.  
XX  
PS Claim 5; SEQ ID NO 4; 146pp; English.  
XX  
CC The present invention describes a combination comprising: (a) a  
CC neuregulin (NRG) protein, a nucleic acid encoding NRG protein and/or function  
CC functional fragment, or an agent that enhances production and/or function  
CC of NRG; and (b) a prophylactic or therapeutic agent for viral  
CC myocarditis, dilated (congestive) cardiomyopathy (DCM), or myocardial  
CC infarction. Also described: (1) a method for preventing, treating or  
CC interfering viral myocarditis, DCM, cardiac toxicity or myocardial  
CC infarction in a mammal by administering a NRG protein, a nucleic acid  
CC encoding the protein, their functional fragment, or an agent that  
CC enhances production and/or function of NRG; (2) a pharmaceutical

CC composition for preventing, treating or delaying viral myocarditis or DCM  
CC in a mammal comprising a NRG protein, a nucleic acid encoding a NRG  
CC protein, their functional fragment, or an agent that enhances production  
CC and/or function of NRG; (3) a kit comprising the combination above or the  
CC composition in a container, and an instruction for using the combination  
CC in preventing, treating or delaying viral myocarditis, DCM or myocardial  
CC infection; and (4) a pharmaceutical composition for preventing, treating  
CC or delaying a disease in a mammal comprising a safety dosage equal to or  
CC less than about 170 U/kg, or in a total regimen equal to or less than  
CC about 3600 U/kg. The combination has cardiant activity. The combination  
CC is useful for preventing, treating or delaying viral myocarditis, DCM,  
CC cardiac toxicity or myocardial infarction. NRG can be used to repair  
CC damaged myocardial cell structure, strengthen connection between these  
CC cells, improve myocardial function and strengthen myocardial biological  
CC effect. The present sequence represents a human neuregulin amino acid  
CC sequence which is used in the exemplification of the present invention.  
CC N.B. The present sequence is designated as SEQ ID NO:2 in the Sequence  
CC Listing, but is given as SEQ ID NO:4 on page 36 of the specification, and  
CC is claimed as SEQ ID NO:4.

SQ Sequence 61 AA;

Query Match 100.0%; Score 342; DB 8; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.4e-26;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLVKCAEKRTFCVNGGECFVWVDLSNPSRYLCKCPNEFTGRCQNYMASFYKAEELY 60  
DB 1 SHLVKCAEKRTFCVNGGECFVWVDLSNPSRYLCKCPNEFTGRCQNYMASFYKAEELY 60

QY 61 Q 61  
DB 61 Q 61

RESULT 2

ID ADF09196 standard; protein; 61 AA.

AC ADF09196;

DT 26-FEB-2004 (first entry)

DE Human neuregulin beta2 fragment #SEQ ID 1.

XX Cardiant; gene therapy; human; neuregulin; viral myocarditis;

KM dilated cardiomyopathy; DCM.

OS Homo sapiens.

PN WO2003099320-A1.

XX 04-DEC-2003.

PF 24-MAY-2002; 2002WO-CN000349.

PR 24-MAY-2002; 2002WO-CN000349.

PA (ZENS-) ZENSUN SHANGHAI SCI TECH LTD.

PI Zhou M.

DR WPI, 2004-035046/03.

DR N-PSDB; ADF09197.

PT New composition for treating viral myocarditis or dilated cardiomyopathy,

PS comprises a neuregulin protein or nucleic acid, an agent that enhances

CC the production or function of neuregulin, and a prophylactic or

CC therapeutic agent.

CC Claim 5; Page 22; 44pp; English.

CC neuregulin protein or its fragment, or a nucleic acid encoding a  
CC neuregulin protein or its fragment, or an agent that enhances production  
CC and/or function of the neuregulin, and an amount of a prophylactic or  
CC therapeutic agent for viral myocarditis or dilated (congestive)  
CC cardiomyopathy (DCM). Also disclosed is a method of preventing, treating  
CC or delaying viral myocarditis or DCM in a mammal. The neuregulin in the  
CC combination carries out its anti-viral myocarditis or anti-DCM activity  
CC via binding with ErbB3-ErbB4 receptors. The prophylactic or therapeutic  
CC agent for viral myocarditis is selected from an antibiotic, a heart  
CC protective agent, an antioxidant and a nutrient for myocardium. The  
CC composition and method of the invention are useful in preventing,  
CC treating or delaying viral myocarditis or dilated cardiomyopathy in  
CC humans. The current sequence represents the amino acid sequence of human  
CC neuregulin beta2 fragment.

SQ Sequence 61 AA;

Query Match 100.0%; Score 342; DB 8; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.4e-26;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLVKCAEKRTFCVNGGECFVWVDLSNPSRYLCKCPNEFTGRCQNYMASFYKAEELY 60  
DB 1 SHLVKCAEKRTFCVNGGECFVWVDLSNPSRYLCKCPNEFTGRCQNYMASFYKAEELY 60

QY 61 Q 61  
DB 61 Q 61

RESULT 3

ID ADF32008 standard; protein; 61 AA.

AC ADF32008;

DT 26-FEB-2004 (first entry)

DE Recombinant plasmid from endonuclease digestion.

XX cardiac toxicity; prophylactic; neuregulin protein; Antiarrhythmic;

KM tumor.

OS Unidentified.

PN WO2003099321-A1.

XX 04-DEC-2003.

PF 18-SEP-2002; 2002WO-CN000664.

PR 24-MAY-2002; 2002WO-CN000349.

PA (ZENS-) ZENSUN SHANGHAI SCI TECH LTD.

PI Zhou M.

DR WPI, 2004-042707/04.

DR N-PSDB; ADF32007.

PT Preventing, treating or delaying cardiac toxicity (e.g. arrhythmia) in

PS humans having malignant tumors comprises administering a neuregulin

CC protein, a nucleic acid encoding neuregulin or an agent enhancing

CC function of neuregulin.

CC Claim 22; SEQ ID NO 2; 36pp; English.

CC The present invention relates to preventing, treating or delaying cardiac

CC toxicity in a mammal comprising administering in vivo prophylactic or

CC therapeutic agent and neuregulin protein or its functional fragment,

CC nucleic acid encoding protein, or agent enhancing production or function

CC of neuregulin, where cardiac toxicity associated with administration of

CC prophylactic or therapeutic agent is prevented, treated or delayed. The



DE EGFL3.  
XX  
XX Glial growth factor; GGF; heregulin; mitogenesis; Schwann cell; tumour;  
KW central nervous system; erbB2 receptor; antiproliferative;  
KW epidermal growth factor; EGF.  
XX  
XX Unidentified.  
XX  
XX WO9403644-A1.  
XX  
XX 17-FEB-1994.  
XX  
XX 10-AUG-1993; 93WO-US007491.  
XX  
XX 10-AUG-1992; 92US-00927337.  
PR 25-SEP-1992; 92US-00951747.  
PR 01-DEC-1992; 92US-00984085.  
PR 29-JAN-1993; 93US-00011396.  
XX  
XX (CAMP-) CAMBRIDGE NEUROSCIENCE INC.  
XX  
XX Gwynne DI, Marchionni M, Mcburney RN,  
PI WPI; 1994-065731/08.  
XX  
XX N-PSDB; AAQ58325.  
DR  
XX  
XX Glial growth factor DNA encoding numerous polypeptide factors used for  
PT inhibiting cell proliferation - for treating carcinoma and nervous  
PT disorders.  
XX  
XX  
XX Disclosure; Fig 41; 178pp; English.  
XX  
XX  
XX The GGF coding segments include regions with EGF-like homology. These EGF  
CC -like domains can be required for the activation of mitogenesis in the  
CC binding reaction between GGF ligands contg. such domains and the erbB2  
CC receptor. Pref. antiproliferative factors are those which lack these EGF-  
CC like domains. (Updated on 10-MAR-2003 to add missing OS field.) (Updated  
CC on 25-MAR-2003 to correct PN field.)  
XX  
XX  
XX Sequence 60 AA;  
SQ  
Query Match 98.5%; Score 337; DB 2; Length 60;  
Best Local Similarity 100.0%; Pred. No. 1e-25;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SHLVKCAEKETFCVNGGECFMYKDLSPSRYLCKCPNEFTGDRCONYMASFYKARELY 60  
1 SHLVKCAEKETFCVNGGECFMYKDLSPSRYLCKCPNEFTGDRCONYMASFYKARELY 60  
DB  
RESULT 7  
AAR67251  
ID AAR67251 standard; protein; 60 AA.  
XX  
XX  
XX AAR67251;  
AC  
XX 25-MAR-2003 (revised)  
DT 15-AUG-1995 (first entry)  
XX  
XX Human epidermal like growth factor 3 (EGFL3).  
XX  
XX  
KW Epidermal like growth factor 3; mammalian muscle cell treatment; EGF3.  
KW skeletal; cardiac; smooth; acetylcholine receptor deficiency; EGFL3.  
XX  
XX Homo sapiens.  
XX  
XX WO9426298-A1.  
XX  
XX 24-NOV-1994.  
XX  
XX 06-MAY-1994; 94WO-US005083.  
PF  
XX 06-MAY-1993; 93US-00059022.  
PR

PR 08-MAR-1994; 94US-00209204.  
XX  
XX  
XX (CAMP-) CAMBRIDGE NEUROSCIENCE.  
XX  
XX Sklar R, Marchionni M, Gwynne DI,  
PI WPI; 1995-006353/01.  
XX  
XX DR N-PSDB; AAQ74916.  
XX  
XX  
XX Treating mammalian muscle diseases and disorders - by admin. of GGF2 and  
PT other specified polypeptide(s) which bind the p185erbB2 receptor.  
XX  
XX  
XX Claim 35; Page 149; 241pp; English.  
XX  
XX  
XX AAQ74916 encodes AAR67251 human epidermal like growth factor 3 (EGFL3).  
CC The glial cell mitogenic activity of EGFL3 can be used to treat a variety  
CC of mammalian skeletal, cardiac and smooth muscle diseases, including  
CC acetylcholine receptor deficiency. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
XX  
XX Sequence 60 AA;  
SQ  
Query Match 98.5%; Score 337; DB 2; Length 60;  
Best Local Similarity 100.0%; Pred. No. 1e-25;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SHLVKCAEKETFCVNGGECFMYKDLSPSRYLCKCPNEFTGDRCONYMASFYKARELY 60  
1 SHLVKCAEKETFCVNGGECFMYKDLSPSRYLCKCPNEFTGDRCONYMASFYKARELY 60  
DB  
RESULT 8  
AAR96077  
ID AAR96077 standard; peptide; 60 AA.  
XX  
XX  
XX AAR96077;  
AC  
XX 27-AUG-1996 (first entry)  
DT  
XX  
XX  
XX Epidermal growth factor-like domain GGF peptide EGFL3.  
XX  
XX  
XX Glial growth factor; GGF; human; hGGF2; Schwann cell; mitogenesis; GGF-1;  
KW glial cell; therapy; neuregulin; heregulin; cellular communication; hEGF;  
KW vertebrate; neuron; muscle cell; nervous system; neurotrophic agent;  
KW matrix molecule; protease; protease inhibitor; neurological disorder;  
KW peripheral neuropathy; amyotrophic lateral sclerosis; nerve injury;  
KW spinal muscular atrophy; Alzheimer's disease; spinal cord injury;  
KW epidermal growth factor.  
XX  
XX  
XX Synthetic.  
XX  
XX  
XX WO9615812-A1.  
XX  
XX 30-MAY-1996.  
XX  
XX 16-NOV-1995; 95WO-US014974.  
PF  
XX 17-NOV-1994; 94US-00341018.  
PR  
XX  
XX (CAMP-) CAMBRIDGE NEUROSCIENCE INC.  
XX  
XX  
XX Gwynne DI, Mahanthappa NK, Marchionni MA, Bermingham-McDonogh O,  
PI Goldin SM, Mcburney RN,  
XX  
XX WPI; 1996-268341/27.  
XX  
XX N-PSDB; AAT30991.  
XX  
XX  
XX Use of neuregulin to affect cellular communication in a vertebrate - by  
PT admin. of a neuregulin or neuregulin DNA, used to treat neurological  
PT disorders, e.g. Alzheimer's disease, peripheral neuropathy etc.  
XX  
XX  
XX Disclosure; Fig 20; 111pp; English.  
XX



Query Match 98.5%; Score 337; DB 2; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 1e-25;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLVKAEKREKTCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYMASFYKAEELY 60  
 |||||  
 DB 1 SHLVKAEKREKTCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYMASFYKAEELY 60

## RESULT 11

AAB12601  
 ID AAB12601 standard; peptide; 58 AA.

XX AAB12601;

XX 09-NOV-2000 (first entry)

DE Human neuregulin beta 2 isoform fragment peptide sequence SEQ ID NO:2.

XX Human; neuregulin; neuregulin beta 2 isoform; epithelial growth factor;

KW EGF; cardiac muscle; cardiomyocyte; growth; differentiation; NRG;

XX heart disease; cardiac; cardioprotective.

OS Homo sapiens.

XX MO200037095-A1.

XX 29-JUN-2000.

XX 21-DEC-1999; 99MO-AU001137.

XX 21-DEC-1998; 98AU-00007850.

XX (CHAN-) CHANG CARDIAC RES INST VICTOR.

XX Zhou M;

XX WPI; 2000-442531/38.

XX N-PSDB; AAA60997.

XX Treating heart disease or heart failure comprises administering

PT neuregulin to enhance cardiomyocyte growth and/or differentiation.

XX Disclosure; Page 11; 44pp; English.

XX The present invention describes a method for inducing cardiomyocyte

CC growth and/or differentiation comprising exposing the cell to neuregulin

CC (NRG) with subsequent activation of the MAP kinase pathway. Neuregulin

CC increases cardiac muscle cell differentiation and organization of

CC sarcomeric and cytoskeletal structures and also enhances cell-to-cell

CC adhesion. The method is useful in the treatment or management of heart

CC disease or failure in a mammal. The present sequence represents a human

CC neuregulin beta 2 isoform peptide fragment, containing the epithelial

CC growth factor (EGF) like domain and the receptor binding domain

XX Sequence 58 AA;

XX Query Match 92.4%; Score 316; DB 3; Length 58;

XX Best Local Similarity 96.7%; Pred. No. 1.1e-23;

XX Matches 58; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 SHLVKAEKREKTCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYMASFYKAEELY 60  
 |||||  
 DB 1 SHLVKCA--EKTCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYMASFYKAEELY 58

RESULT 12

ADY28292

ID ADY28292 standard; protein; 57 AA.

XX ADY28292;

XX 05-MAY-2005 (first entry)

XX Novel ErbB ligand-related EGF domain protein region SeqID15.

KW ErbB ligand; EGF domain; neuroprotective; cytoskeletal; vasotropic;

KW vulnary; antiangiogenic; neuroleptic; gene therapy; ErbB receptor;

KW hyperproliferation; neurological disease; psychiatric disorder;

XX angio genesis disorder; restenosis; wound healing; neurological disease.

OS Homo sapiens.

XX WO2005017096-A2.

XX 24-FEB-2005.

XX 19-AUG-2004; 2004WO-IL000759.

XX 19-AUG-2003; 2003US-0495898P.

XX (AGOS-) AGOS BIOTECH LTD.

XX Harari D;

XX WPI; 2005-173275/18.

XX New polypeptide comprising a splice variant of an ErbB ligand encoded by

XX differential exon usage comprising a truncated EGF domain devoid of the C

XX loop of the EGF domain, useful in preparing a composition for treating

XX e.g., restenosis.

XX Example; SEQ ID NO 15; 158pp; English.

XX This invention relates to a novel polypeptide which comprises a splice

XX variant of an ErbB ligand encoded by differential exon usage comprising a

XX truncated EGF domain devoid of the C-loop of the EGF domain. The

XX invention may be useful for the development of compounds with a

XX neuroprotective, cytoskeletal, vasotropic, vulnary, antiangiogenic or

XX neuroleptic activity whilst the disclosed sequences may prove useful for

XX gene therapy. The polypeptide is useful in preparing a composition for

XX treating a disease or disorder related to an ErbB receptor or to

XX pathological activity of at least one ErbB receptor. For example

XX neoplastic, hyperproliferative, neurological or psychiatric disorders,

XX angiogenesis, restenosis, wound or neurological injuries. The present

XX sequence is that of an EGF domain protein region which was used during

XX the illustration of the novel polypeptides of the invention.

XX Sequence 57 AA;

XX Query Match 89.8%; Score 307; DB 9; Length 57;

XX Best Local Similarity 100.0%; Pred. No. 8.4e-23;

XX Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLVKAEKREKTCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYMASFY 54  
 |||||  
 DB 4 SHLVKAEKREKTCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYMASFY 57

RESULT 13

AAE36804

ID AAE36804 standard; protein; 53 AA.

XX AAE36804;

XX 07-AUG-2003 (first entry)

XX Human neuregulin 1 beta EGF-like domain.

XX Epidermal growth factor receptor; EGFR; therapy; psoriasis; carcinoma;

XX cancer; rhabdomyosarcoma; mesothelioma; melanoma; glioblastoma; human;

XX receptor; EGF; neuregulin 1 beta.

XX Homo sapiens.

XX WO2003014159-A1.

```

XX 20-FEB-2003.
PD
XX
XX 05-AUG-2002; 2002WO-AU001042.
PF
XX
XX 03-AUG-2001; 2001AU-00006827.
PR
XX 03-AUG-2001; 2001AU-00006828.
PR
XX 01-NOV-2001; 2001US-0335393P.
PR
XX 01-NOV-2001; 2001US-0336560P.
PR
XX 31-MAY-2002; 2002AU-00002731.
PR
XX 11-JUN-2002; 2002US-0388171P.
XX
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
PA (BIOM-) BIOMOLECULAR RES INST LTD.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PA (LUDW-) LUDWIG INST CANCER RES.
XX
XX Adams TE, Burgess AW, Ellemann TC, Garrett TPJ, Jorissen RN;
PI Lou M, Lovrecz GO, McKern NM, Nice EC, Ward CW;
XX
XX WPI; 2003-268181/26.
DR
XX
XX Selecting or designing compounds that interact with or inhibit formation
PT of active dimers of the EGF receptor family, and useful for the
PT prevention and treatment of disorders, such as psoriasis and cancer of
PT the breast, brain or colon.
XX
XX Disclosure; Fig 2; 354pp; English.
XX
XX The invention relates to a method of selecting or designing a compound
CC that interacts with or inhibits the formation of active dimers of a
CC receptor of the epidermal growth factor receptor (EGFR) family. The
CC methods and compositions of the invention are useful for the prevention
CC and treatment of disorders associated with signalling by a molecule of
CC the EGFR family such as psoriasis and cancer of the pancreas, breast,
CC brain, colon, prostate, ovary, cervix, lung, head and neck, melanoma,
CC rhabdomyosarcoma, mesothelioma, squamous carcinomas of the skin and
CC glioblastomas. The present sequence is epidermal growth factor (EGF) like
CC domain of human neurogulin 1 beta protein. This sequence is used to
CC illustrate the method of the invention
XX
XX Sequence 53 AA;
SQ
XX
XX Query Match 87.7%; Score 300; DB 6; Length 53;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-22;
XX Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SHLVKCAEKETFCVNGGECFMYVDLSNPSRYLCKCPNEFTGDRCONYMASF 53
DB 1 SHLVKCAEKETFCVNGGECFMYVDLSNPSRYLCKCPNEFTGDRCONYMASF 53

```

## RESULT 14

```

ADY28279
ID ADY28279 standard; protein; 56 AA.
XX
XX ADY28279;
AC
XX
XX 05-MAY-2005 (first entry)
DT
XX
XX Novel ErbB ligand-related EGF domain protein region SegID2.
DE
XX
XX ErbB ligand; EGF domain; neuroprotective; cytosolic; vasotrophic;
XX vulnerability; angiogenic; neuroleptic; gene therapy; ErbB receptor;
XX hyperproliferation; neurological disease; psychiatric disorder;
XX angiogenesis disorder; restenosis; wound healing; neurological disease.
XX
XX Homo sapiens.
OS
XX
XX MO2005017096-A2.
XX
XX 24-FEB-2005.
PD
XX

```

```

PF 19-AUG-2004; 2004WO-IL000759.
XX
XX 19-AUG-2003; 2003US-0495898P.
PR
XX
XX (AGOS-) AGOS BIOTECH LTD.
XX
XX Harari D;
XX
XX WPI; 2005-173275/18.
DR
XX
XX New polypeptide comprising a splice variant of an ErbB ligand encoded by
PT differential exon usage comprising a truncated EGF domain devoid of the C
PT -loop of the EGF domain, useful in preparing a composition for treating
PT e.g., restenosis.
XX
XX Disclosure; SEQ ID NO 2; 158pp; English.
XX
XX This invention relates to a novel polypeptide which comprises a splice
CC variant of an ErbB ligand encoded by differential exon usage comprising a
CC truncated EGF domain devoid of the C-loop of the EGF domain. The
CC invention may be useful for the development of compounds with a
CC neuroprotective, cytosolic, vasotrophic, vulnerary, angiogenic or
CC neuroleptic activity whilst the disclosed sequences may prove useful for
CC gene therapy. The polypeptide is useful in preparing a composition for
CC treating a disease or disorder related to an ErbB receptor or to
CC pathological activity of at least one ErbB receptor, for example
CC neoplastic, hyperproliferative, neurological or psychiatric disorders,
CC angiogenesis, restenosis, wound or neurological injuries. The present
CC sequence is that of an EGF domain protein region which was used during
CC the illustration of the novel polypeptides of the invention.
XX
XX Sequence 56 AA;
SQ
XX
XX Query Match 87.7%; Score 300; DB 9; Length 56;
XX Best Local Similarity 100.0%; Pred. No. 4e-22;
XX Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SHLVKCAEKETFCVNGGECFMYVDLSNPSRYLCKCPNEFTGDRCONYMASF 53
DB 4 SHLVKCAEKETFCVNGGECFMYVDLSNPSRYLCKCPNEFTGDRCONYMASF 56

```

## RESULT 15

```

AAB36802
ID AAB36802 standard; protein; 56 AA.
XX
XX AAB36802;
AC
XX
XX 16-FEB-2001 (first entry)
DT
XX
XX Protein #9.
DE
XX
XX Heregulin; ErbB receptor; transplantation; cancer;
XX nervous system disease; musculature; epithelium.
XX
XX Homo sapiens.
OS
XX
XX US6136558-A.
XX
XX 24-OCT-2000.
PD
XX
XX 09-FEB-1998; 98US-00020880.
PF
XX
XX 10-FEB-1997; 97US-0037581P.
PR
XX
XX (GENTH ) GENENTECH INC.
PA
XX
XX Jones JT, Fairbrother WJ, Ballinger MD, Wells JA, Sliwkowski MX;
XX
XX WPI; 2000-678767/66.
XX
XX New variants of heregulin, useful e.g. for treating cancer, comprises
PT specific amino acid alterations that increase affinity for ErbB

```

```

PT receptors.
XX
PS Disclosure; Col 89-90; 58pp; English.
XX
CC The present invention relates to variants of heregulin that can bind to
CC an ErbB receptor and include a portion of the 175-230 region of native
CC human heregulin-beta1. The variants may be used to promote ex vivo
CC survival, proliferation and differentiation of cells, particularly when
CC intended for transplantation. They may also be used to treat a wide range
CC of cancers and diseases of the nervous system, musculature and epithelium
XX
SQ Sequence 56 AA;

```

```

Query Match      87.1%; Score 298; DB 3; Length 56;
Best Local Similarity 96.3%; Pred. No. 6.3e-22;
Matches 52; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 SHLVKCAEKKEKTCVNGGECFMYKDLSPSRYLCKCPNEFTGDRCONVWASFY 54
   |||||
Db 3 SHLVKCAEKKEKTCVNGGECFMYKDLSPSRYLCKCPNEFTGDRCONVWASFY 56

```

Search completed: January 26, 2006, 12:42:11  
 Job time : 75 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 26, 2006, 12:33:27 ; Search time 16 seconds

(without alignments)  
366.826 Million cell updates/sec

Title: US-09-980-672-2

Perfect score: 342  
Sequence: 1 SHLVKCAKEKTEFCVNGSEC.....GDRCONVMASFYAEELYQ 61

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 263416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 16431

Minimum DB seq length: 0  
Maximum DB seq length: 61

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:\*

1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122.5	35.8	57	2	PC4415
2	77.5	22.7	53	2	S17294
3	69	20.2	46	2	UT0747
4	68	19.9	50	2	A61215
5	68	19.9	50	2	A48545
6	59.5	17.4	43	2	A48998
7	46	13.5	61	2	UX0309
8	43.5	12.7	53	2	S29214
9	43.5	12.7	58	2	A37039
10	42.5	12.6	56	2	E31440
11	42.5	12.4	49	2	S29173
12	42.5	12.4	49	2	F70221
13	42	12.3	46	2	B31441
14	41	12.0	56	2	B61494
15	40.5	11.8	19	2	A31252
16	40.5	11.8	38	2	P0187
17	40.5	11.8	48	2	G53613
18	40.5	11.8	46	2	I38217
19	40.5	11.8	49	2	D70228
20	40.5	11.8	55	2	T10344
21	40.5	11.8	59	2	T08149
22	40.5	11.8	60	2	D97932
23	40	11.7	37	2	A59401
24	40	11.7	56	2	E31438
25	40	11.7	56	2	D31440
26	40	11.7	56	2	F61493
27	40	11.7	57	1	T2NJR
28	40	11.7	58	1	SKMD1S
29	40	11.7	61	2	T13448

30	39.5	11.5	37	2	A60963	charybotoxin 1 [v
31	39.5	11.5	49	2	S29215	neurotoxin Tx2 - s
32	39.5	11.5	55	2	S30496	protein kinase Mpx
33	39.5	11.5	58	2	F75180	hypothetical prote
34	39	11.4	20	2	A48394	major fat-globule
35	39	11.4	38	1	C35030	cutaroxin III - f
36	39	11.4	48	2	S29216	neurotoxin Tx2 - s
37	39	11.4	54	2	A61494	ovomucoid (PSTI-cy
38	39	11.4	54	2	H61493	ovomucoid (PSTI-cy
39	39	11.4	54	2	C31443	ovomucoid, third d
40	39	11.4	56	2	A31445	ovomucoid, third d
41	39	11.4	56	2	H31439	ovomucoid, third d
42	39	11.4	56	2	E31437	ovomucoid, third d
43	39	11.4	56	2	E31442	ovomucoid, third d
44	39	11.4	56	2	I31439	ovomucoid, third d
45	39	11.4	56	2	G61493	ovomucoid (PSTI-cy

#### ALIGNMENTS

##### RESULT 1

PC4415  
ErbB kinase activator beta, brain and thymus - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 10-Dec-1997 #sequence\_revision 10-Dec-1997 #text\_change 08-Sep-2002  
C/Accession: PC4415  
R/Higashiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.; Miy, J. Biochem. 122, 675-680, 1997  
A/Title: A novel brain-derived member of the epidermal growth factor family that inter-  
A/Reference number: J05700; MUID:98006324; PMID:9348101  
A/Accession: PC4415  
A/Status: nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-57 <HIG>  
A/Cross-references: UNIPARC:UPI00000170767; DDBJ:D89997; NID:g2605633; PIDN:BAA2346.1;  
A/Experimental source: PC-12 cell  
C/Comment: This protein is a member of the epidermal growth factor family. It is functi-  
ating the differentiation of MDA-MB-453 cells.  
C/Superfamily: human ErbB kinase activator alpha, brain and thymus; EGF homology; Immur  
F/1-25/Domain: EGF homology (fragment) <EGF>

Query Match 35.8%; Score 122.5; DB 2; Length 57;  
Best Local Similarity 50.0%; Pred. No. 2.8e-07;  
Matches 22; Conservative 8; Mismatches 11; Indels 3; Gaps 1;

Cy 18 GECFMVMDLSRPSRYLCKPWEFTGDRCONVMASFYAEELYQ 61  
Db 1 GVCYYIRISINQLS---CKCPVGYTGDRCONVPMVNFSAEELYQ 41

##### RESULT 2

S17294  
epidermal growth factor - pig (fragment)  
C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C/Accession: S17294  
R/Pascall, J.C.; Jones, D.S.C.; Doel, S.M.; Clements, J.M.; Hunter, M.; Fallon, T.; Ed  
J. Mol. Endocrinol. 6, 63-70, 1991  
A/Title: Cloning and characterization of a gene encoding pig epidermal growth factor.  
A/Reference number: S17294; MUID:91197366; PMID:2015058  
A/Accession: S17294  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-53 <PAS>  
A/Cross-references: UNIPROT:Q00968; UNIPARC:UPI000002D1A4; EMBL:X59516; NID:g1940; PIDN  
C/Superfamily: epidermal growth factor precursor; EGF homology; LDL receptor ITID-conta  
F/6-42/Domain: EGF homology <EGF>

Query Match 22.7%; Score 77.5; DB 2; Length 53;  
Best Local Similarity 27.9%; Pred. No. 0.038; Indels 3; Gaps 1;  
Matches 12; Conservative 11; Mismatches 17;





## RESULT 13

B31441

Ovomucoid, third domain - gray francolin (fragment)

C/Species: Francolinus pondicerianus (gray francolin)

C/Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #ext\_change 09-Jul-2004

C/Accession: B31441

R/Laskowski Jr., M.; Kato, I.; Ardelt, W.; Cook, J.; Denton, A.; Empe, M.W.; Kohn, W.J.

Biochemistry 26, 202-221, 1987

A/Title: Ovomucoid third domains from 100 avian species: isolation, sequences, and hyper

A/Reference number: A90515; MUID:87157615; PMID:3828298

A/Accession: B31441

A/Molecule type: protein

A/Residues: 1-56 &lt;IAS&gt;

A/Cross-references: UNIPROT:P05598; UNIPARC:UPI000012D783

A/Note: the authors designate this sequence with the code OMGRF3

C/Superfamily: ovomucoid; Kazal proteinase inhibitor homology

C/Keywords: egg white; glycoprotein; serine proteinase inhibitor

F/6-56/Domain: Kazal proteinase inhibitor homology &lt;KPI&gt;

F/8-38,16-35,24-56/Disulfide bonds: #status predicted

F/45/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.3%; Score 42; DB 2; Length 56;

Best Local Similarity 27.5%; Pred. No. 4.6e+02;

Matches 14; Conservative 6; Mismatches 17; Indels 14; Gaps 2;

QY 4 VKCAEKETFCVNGGECFMVKDLSNPRYLCKCPNEFTGDRQ--NYVMAS 52

DB 6 VDCSEYKPPDC-----TTERPLCGSDNKTGKNCNCAVNES 44

## RESULT 14

B61494

Ovomucoid (PRTI-type proteinase inhibitor), third domain - Congo peafowl (fragment)

C/Species: Afropavo congenis (Congo peafowl)

C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #ext\_change 09-Jul-2004

C/Accession: B61494; B31115

R/Laskowski Jr., M.; Apostol, I.; Ardelt, W.; Cook, J.; Gilletto, A.; Kelly, C.A.; Lu, W.

J. Protein Chem. 9, 715-725, 1990

A/Title: Amino acid sequences of ovomucoid third domain from 25 additional species of b

A/Reference number: A61492; MUID:91158808; PMID:2073323

A/Accession: B61494

A/Molecule type: protein

A/Residues: 1-56 &lt;IAS&gt;

A/Cross-references: UNIPROT:P52258; UNIPARC:UPI000012D75A

C/Superfamily: ovomucoid; Kazal proteinase inhibitor homology

C/Keywords: egg white; glycoprotein; serine proteinase inhibitor

F/6-56/Domain: Kazal proteinase inhibitor homology &lt;KPI&gt;

F/8-38,16-35,24-56/Disulfide bonds: #status predicted

F/45/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.0%; Score 41; DB 2; Length 56;

Best Local Similarity 27.5%; Pred. No. 6.1e+02;

Matches 14; Conservative 6; Mismatches 17; Indels 14; Gaps 2;

QY 4 VKCAEKETFCVNGGECFMVKDLSNPRYLCKCPNEFTGDRQ--NYVMAS 52

DB 6 VDCSEYKPPAC-----TWQRPLCGSDNKTGKNCNCAVNES 44

## RESULT 15

A31252

metallothionein I - yeast (Candida glabrata) (fragment)

C/Species: Candida glabrata

C/Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #ext\_change 09-Jul-2004

C/Accession: A31252

R/Mehra, R.K.; Tarbet, E.B.; Gray, W.R.; Winge, D.R.

Proc. Natl. Acad. Sci. U.S.A. 85, 8815-8819, 1988

A/Title: Metal-specific synthesis of two metallothioneins and gamma-glutamyl peptides in

A/Reference number: A94212; MUID:89057829; PMID:3194392

A/Molecule type: protein

A/Residues: 1-19 &lt;MEH&gt;

A/Cross-references: UNIPROT:P5113; UNIPARC:UPI0000177CA5

C/Superfamily: metallothionein

Query Match 11.8%; Score 40.5; DB 2; Length 19;

Best Local Similarity 57.1%; Pred. No. 2.6e+02;

Matches 8; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 34 CKCPNEFTGDRQCN 47

DB 4 CKCPN---GCSPN 14

Search completed: January 26, 2006, 12:43:55  
Job time: 17 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model1

Run on: January 26, 2006, 12:31:01 ; Search time 67 seconds

(without alignments)  
642,347 Million cell updates/sec

Title: US-09-980-672-2

Perfect score: 342  
Sequence: 1 SHLVKCAKEKTEFCVNGSEC.....GDRCONVMAFYKAEELTYG 61

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 129292

Minimum DB seq length: 0  
Maximum DB seq length: 61

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	160	46.8	58	2	086WJ0 HUMAN
2	141.5	41.4	54	2	0810X1 MOUSE
3	74	21.6	42	2	08WY1 HUMAN
4	70.5	20.6	53	2	06QBS2 HUMAN
5	70	20.5	34	2	068D87 HUMAN
6	70	20.5	36	2	072663 HUMAN
7	68	19.9	50	1	TGFA_RABIT
8	68	19.9	50	2	Q7M0A9 MESAU
9	66	19.3	50	2	Q6QBS1 HUMAN
10	61.5	18.0	59	2	Q4T175 TETNG
11	59	17.3	57	2	Q5IEC4 HUMAN
12	58.5	17.1	44	2	Q4S14 TETNG
13	55	16.1	39	2	Q9MZP7 BOVIN
14	55	16.1	61	2	Q84KT0 CAEOL
15	53.5	15.6	52	2	Q9TX97 CAEOL
16	51	14.9	37	2	Q5VVG4 HUMAN
17	50	14.6	57	2	Q64QMS BACFR
18	49.5	14.5	36	2	Q4T2A0 TETNG
19	49.5	14.5	42	1	SEK1_CENGR
20	48.5	14.2	37	2	Q6L8Y4 HUMAN
21	46.5	13.6	51	2	Q9CQH4 MOUSE
22	46.5	13.6	55	2	Q5T3C9 HUMAN
23	46	13.5	57	2	Q95S09 DROME
24	46	13.5	61	1	IBB_BRVVA
25	45	13.2	34	2	Q8F634 LEPIN
26	45	13.2	39	2	O18628 SCHMA
27	45	13.2	54	2	Q7Y500 BPR69
28	45	13.2	56	2	Q4XQW9 PLACH
29	45	13.2	58	2	Q69BD0 CAMUE
30	45	13.2	58	2	Q69B10 CAMCO
31	45	13.2	60	2	Q4ZU96_PSESY

32	45	13.2	60	2	0883A4 PSESM
33	44.5	13.0	42	1	SEK1_CENRL
34	44.5	13.0	47	2	Q934J1 CARPI
35	44.5	13.0	48	2	Q55AE1 dictyostell
36	44	12.9	37	2	Q86B27 9CAEN
37	44	12.9	54	1	TX36_PHOKE
38	44	12.9	56	2	Q4HDT4 CAMCO
39	44	12.9	59	2	Q5YA52 9CAUD
40	44	12.9	60	2	Q4KE11_PSEFS
41	43.5	12.7	58	1	MT1_HOMAM
42	43.5	12.7	58	2	Q95P38 HOMAM
43	43	12.6	40	2	Q5M419 STRT2
44	43	12.6	47	2	Q91X04 9ENNO
45	43	12.6	51	2	Q8DT16_STRMU

## ALIGNMENTS

```

RESULT 1
086WJ0 HUMAN
ID 086WJ0 HUMAN PRELIMINARY; PRT; 58 AA.
AC 086WJ0;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Neurigin 1 isoform 4 (Fragment).
GN Name=NRG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22993650; PubMed=14632199;
RX DOI=10.1046/j.1523-1747.2003.12522.x;
RA Stove C., Stove V., Derycke L., Van Marck V., Mareel M., Bracke M.;
RT "The heregulin/human epidermal growth factor receptor as a new growth
factor system in melanoma with multiple ways of deregulation.";
RL J. Invest. Dermatol. 121:802-812(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Stove C.P., Stove V.V., Mareel M.M., Bracke M.E.;
RL Submitted (DEC-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY207002; AAC49724.1; -; mRNA.
DR HSSP; Q12780; 1HAE.
DR SMR; 086WJ0: 1-47.
DR InterPro; IPR007742; EGF_2.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00008; EGF_1.
DR SMART; SM00181; EGF_1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
KW EGF-like domain.
FT NON TER 1 1
SQ SEQUENCE 58 AA; 6299 MW; 48F31F0CE45A1FB CRC64;

Query Match 46.8%; Score 160; DB 2; Length 58;
Best Local Similarity 80.6%; Pred. No. 1.7e-11;
Matches 29; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 14 CVNGGECFMYVDLSNPSRYLCKCPNPTGRCQYV 49
Db 1 CVNGGECFMYVDLSNPSRYLCKCPNPTGRCQYV 36

RESULT 2
0810X1 MOUSE
ID 0810X1_MOUSE PRELIMINARY; PRT; 54 AA.
AC 0810X1;

```

```

DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Neuregulin 2-beta (Fragment).
CN Name=Nrg2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CD-1; TISSUE=Olfactory bulb;
RX PubMed=15039062; DOI=10.1016/j.pep.2003.12.012;
RA Mautino B., Dalla Costa L., Gambirotta G., Petroreau I., Fasolo A.,
RA Dati C.;
RT "Bioactive recombinant neuregulin-1, -2, and -3 expressed in
RT Escherichia coli."
RL Protein Expr. Purif. 35:25-31(2004).
DR EMBL; AY227026; AA072523.1; -; mRNA.
DR HSSP; P01133; 1JL9.
DR MGI; MGI:1098246; Nrg2.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00008; EGF_1.
DR SMART; SM00181; EGF_1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
KW EGF-like domain.
FT NON_TER 1 54
FT NON_TER 54 54
SQ SEQUENCE 54 AA; 6019 MW; C25NA17AD0BA59A CRC64;

Query Match 41.4%; Score 141.5; DB 2; Length 54;
Best Local Similarity 47.1%; Pred. No. 2.6e-09;
Matches 24; Conservative 10; Mismatches 14; Indels 3; Gaps 1;

Qy 5 KCAEKETFCVNGGECFMVNDLSNPSRYLCKPNEFTGDRCONVMASFYK 55
Db 1 KCNETAKSYCVNGVCYIRGINLS---CKCPGYIGDRCCQAPAMNFSK 48

RESULT 3
08MWY1_HUMAN PRELIMINARY; PRT; 42 AA.
ID 08MWY1_HUMAN PRELIMINARY; PRT; 42 AA.
AC 08MWY1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE CBH1 isoform III (Crumbs homolog 1) (Drosophila) (Fragment).
GN Name=CBH1; ORFNames=RP11-53124.1-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99438399; PubMed=10508521; DOI=10.1038/13848;
RA den Hollander A.I., ten Brink J.B., de Kok Y.J.M., van Soest S.,
RA van den Born L.I., van Driel M.A., van de Pol D.J.R., Payne A.M.,
RA Bhattacharya S.S., Kellner U., Hoyng C.B., Westerveld A.,
RA Brunner H.G., Bleeker-Wagemakers E.M., Deutman A.F.,
RA Mecklenhove J.R., Cremers F.P.M., Bergen A.A.B.;
RT "Mutations in a human homologue of Drosophila crumbs cause retinitis
RT pigmentosa (RP12).";
RL Nat. Genet. 23:217-221(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21592405; PubMed=11734541; DOI=10.1093/hmg/10.24.2767;
RA den Hollander A.I., Johnson K., de Kok Y.J.M., Klebes A.,

```

```

RA Brunner H.G., Knust B., Cremers F.P.M.;
RT "CRB1 has a cytoplasmic domain that is functionally conserved between
RT human and Drosophila.";
RT Hum. Mol. Genet. 10:2767-2773(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Smith M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Holt K.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY043323; AL10680.1; -; mRNA.
DR EMBL; AL136322; CA116645.1; -; Genomic_DNA.
DR EMBL; AL139136; CA115310.1; -; Genomic_DNA.
DR EMBL; AL139136; CA116645.1; JOINED; Genomic_DNA.
DR EMBL; AL136322; CA115310.1; JOINED; Genomic_DNA.
DR HSSP; P08709; 1BF9.
DR Ensemble; ENSG00000134376; Homo sapiens.
DR GO; GO:0005509; F-actin filament binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca_bd.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF_1.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00179; EGF_CA; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
KW EGF-like domain.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 42 AA; 4630 MW; 407D112FAF090D15 CRC64;

Query Match 21.6%; Score 74; DB 2; Length 42;
Best Local Similarity 40.5%; Pred. No. 0.25;
Matches 17; Conservative 6; Mismatches 11; Indels 8; Gaps 3;

Qy 5 KCAEKETFCVNGGECFMVNDLSNPSRYLCKPNEFTGDRCCQ 46
Db 6 ECASDP---CVNGGLC---QDLIN--KFCGLCVAFAGEKCE 39

RESULT 4
06QBS2_HUMAN PRELIMINARY; PRT; 53 AA.
ID 06QBS2_HUMAN PRELIMINARY; PRT; 53 AA.
AC 06QBS2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Epidermal growth factor (Fragment).
GN Name=EGF;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nguyen N.L., Do Q.H., Vu M.T., Nguyen B.N., Phan V.C.;
RT "Cloning of a gene encoding for a human epidermal growth factor.";
RL Y Hoc Viet Nam 298:43-45(2004).
DR EMBL; AY548762; AAS83395.1; -; mRNA.
DR HSSP; P01132; 1A3P.
DR SMR; 06QBS2; 3-50.
DR InterPro; IPR001336; EGF_1.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00008; EGF_1.
DR PRINTS; PR00009; EGFTRC.

```

DR SMART; SM00181; EGF; 1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS50026; EGF\_3; 1.  
 KM EGF-like domain; Growth factor.  
 FT NON\_TER 1 1  
 FT NON\_TER 53 53  
 SO SEQUENCE 53 AA; 6222 MW; 7D6A806D873B071 CRC64;

Query Match 20.6%; Score 70.5; DB 2; Length 53;  
 Best Local Similarity 28.6%; Pred. No. 0.81;  
 Matches 12; Conservative 9; Mismatches 18; Indels 3; Gaps 1;

QY 5 KCAKEKTEFCVNGGECFVMDLSPRYLCKCPHEFGDRQ 46  
 DB 5 ECLPSHDGCLHDGCMVTEAL--DKYACNCVGVYGERQ 43

RESULT 5  
 Q68D87 HUMAN PRELIMINARY; PRT; 34 AA.  
 AC Q68D87;  
 DT 25-OCT-2004 (TREMBlrel. 28, Created)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
 DE Hypothetical protein DKFZp79N0541 (Fragment).  
 GN Name=DKFZp79N0541;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo  
 NC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Liver;  
 RG The German CDNA Consortium;  
 RA Koehler K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Rodo G., Han M., Wiemann S.;  
 RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CR749519; CAH18333.1; -; mRNA.  
 KM Hypothetical protein.  
 FT NON\_TER 34 34  
 FT SEQUENCE 34 AA; 3678 MW; 1FB19C9A9FC42240 CRC64;

Query Match 20.5%; Score 70; DB 2; Length 34;  
 Best Local Similarity 35.7%; Pred. No. 0.6;  
 Matches 10; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 2 HLYKAEKTEFCVNGGECFVMDLSP 29  
 DB 5 HEEPCGSHKSFCLNGCLCYVPIPIPS 32

RESULT 6  
 Q72663 HUMAN PRELIMINARY; PRT; 36 AA.  
 AC Q72663;  
 DT 01-OCT-2003 (TREMBlrel. 25, Created)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Hypothetical protein DKFZp79N1944.  
 GN Name=DKFZp79N1944;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo  
 NC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Rodo G., Han M., Wiemann S.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BX538100; CAD98015.1; -; mRNA.  
 KM Hypothetical protein.  
 SO SEQUENCE 36 AA; 3963 MW; 56287FB19C9A9FC4 CRC64;

Query Match 20.5%; Score 70; DB 2; Length 36;  
 Best Local Similarity 35.7%; Pred. No. 0.64;  
 Matches 10; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 2 HLYKAEKTEFCVNGGECFVMDLSP 29  
 DB 5 HEEPCGSHKSFCLNGCLCYVPIPIPS 32

RESULT 7  
 TGFA RABIT STANDARD; PRT; 50 AA.  
 ID TGFA RABIT  
 AC P98138;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Transforming growth factor alpha (TGF-alpha) (EGF-like TGF) (ETGF)  
 DE (TGF type 1) (Fragment).  
 GN Name=TGFA;  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;  
 OC Oryctolagus.  
 NC NCBI\_TaxID=9986;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=93150169; PubMed=8426908; DOI=10.1016/0167-0115(93)90405-W;  
 RA Goldring J.R., Tsunoda Y., Stoch S.A., Coffey R.J., Modlin I.M.,  
 RT "Transforming growth factor-alpha (TGF alpha) inhibition of parietal  
 cell secretion: structural requirements for activity.";  
 RL Regul. Pept. 43:37-47(1993).  
 CC -1- FUNCTION: Inhibitor of acid secretion. Inhibitor of aminopyrine  
 uptake in parietal cells (in vitro).  
 CC -1- SUBUNIT: Interacts with the PDZ domains of SDCBP and SNTAL. The  
 interaction with SDCBP is required for the targeting to the cell  
 surface (By similarity).  
 CC -1- TISSUE SPECIFICITY: Gastric parietal cells.  
 CC -1- SIMILARITY: Contains 1 EGF-like domain.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

-----  
 CC EMBL; M86827; AAA73200.1; -; mRNA.  
 DR PIR; A48545; A48545.  
 DR HSP; P01135; 3TGF.  
 DR SMR; P98138; 2-50.  
 DR InterPro; IPR001336; EGF\_1.  
 DR InterPro; IPR007742; EGF\_2.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR006210; IEGF.  
 DR Pfam; PF00008; EGF; 1.  
 DR PRINTS; PRO0009; EGFTEF.  
 DR SMART; SM00181; EGF; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS50026; EGF\_3; 1.  
 KM EGF-like domain; Growth factor; Mitogen.  
 FT DOMAIN 4 44 EGF-like.  
 FT DISULFID 8 21 By similarity.  
 FT DISULFID 16 32 By similarity.  
 FT DISULFID 34 43 By similarity.  
 FT NON\_TER 1 1  
 FT NON\_TER 50 50  
 FT SEQUENCE 50 AA; 5565 MW; BDD508F4053625DB CRC64;  
 Query Match 19.9%; Score 68; DB 1; Length 50;

Best Local Similarity 27.7%; Pred. No. 1.5;  
Matches 13; Conservative 11; Mismatches 19; Indels 4; Gaps 1;

OY 1 SHLVKAEKEKTEFCVNGEGCFMWKDLSPSRYLCKCPNEFTGDRCON 47  
DB 3 SHFNQCPDSDHTQFCFHGTCTFLVOE----DKPACVCHSGVYGARCEH 45

## RESULT 8

ID Q7M0A9\_MESAU PRELIMINARY; PRT; 50 AA.  
AC Q7M0A9;  
DT 01-MAR-2004 (TReMBLrel. 26, Created)  
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)  
DE Transforming growth factor alpha precursor (Fragment).  
OS Mesocricetus auratus (Golden hamster).  
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Cricetinae; Mesocricetus.  
OX NCBI\_TaxID=10036;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=9183613; Pubmed=2009597;  
RA Chiang T., McBride J., Chou M.Y., Nishimura I., Wong D.T.W.;  
RT "Molecular cloning of the complementary DNA encoding for the hamster  
TGF-alpha mature peptide."  
RL Carcinogenesis 12:529-532(1991).  
DR PIR; A61215; A61215.  
DR HSSP; P01135; IMOX.  
DR SMR; Q7M0A9; 2-50.  
DR InterPro; IPR001336; EGF\_1.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR006209; EGF\_like.  
DR Pfam; PF00008; EGF\_1.  
DR PRINTS; PR00009; EGF\_TGF.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS50026; EGF\_3; 1.  
KW Growth factor.

FT NON\_TER 1 1  
FT NON\_TER 50 50  
SQ SEQUENCE 50 AA; 5580 MW; FCD508B454732000 CRC64;  
Query Match 19.9%; Score 68; DB 2; Length 50;  
Best Local Similarity 27.7%; Pred. No. 1.5;  
Matches 13; Conservative 11; Mismatches 19; Indels 4; Gaps 1;

OY 1 SHLVKAEKEKTEFCVNGEGCFMWKDLSPSRYLCKCPNEFTGDRCON 47  
DB 3 SHFNQCPDSDHTQFCFHGTCTFLVOE----DKPACVCHSGVYGARCEH 45

## RESULT 9

ID Q6QBS1\_HUMAN PRELIMINARY; PRT; 50 AA.  
AC Q6QBS1;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE Transforming growth factor alpha (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.

RA Phan V.C., Nguyen B.N., Do Q.H.;  
RT "Molecular cloning and sequence analysis of the transforming growth  
RT factor alpha gene from Homo sapiens placenta."  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY548763; AAS83396.1; -, mRNA.

DR SMR; Q6QBS1; 2-50.  
DR InterPro; IPR001336; EGF\_1.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR006209; EGF\_like.  
DR Pfam; PF00008; EGF\_1.  
DR PRINTS; PR00009; EGF\_TGF.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS50026; EGF\_3; 1.  
KW Growth factor.

FT NON\_TER 1 1  
FT NON\_TER 50 50  
SQ SEQUENCE 50 AA; 5552 MW; BDD508E5053634DB CRC64;  
Query Match 19.3%; Score 66; DB 2; Length 50;  
Best Local Similarity 27.7%; Pred. No. 2.7;  
Matches 13; Conservative 10; Mismatches 20; Indels 4; Gaps 1;

OY 1 SHLVKAEKEKTEFCVNGEGCFMWKDLSPSRYLCKCPNEFTGDRCON 47  
DB 3 SHFNQCPDSDHTQFCFHGTCTFLVOE----DKPACVCHSGVYGARCEH 45

## RESULT 10

ID Q4T175\_TETNG PRELIMINARY; PRT; 59 AA.  
AC Q4T175;  
DT 13-SEP-2005 (TReMBLrel. 31, Created)  
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)  
DE Chromosome undetermined SCAF2358, whole genome shotgun sequence.  
DE (Fragment).  
GN ORFNames=GSTENG00000101001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.

RA Jallou O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
RA Mucadi E., Bouneau L., Fischer C., Ozouf-Coataz C., Bernot A.,  
RA Nicand S., Jaffe D., Fisher S., Lutfalla G., Dosat C., Segurens B.,  
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Casseil L., Katinka M., Vacherie B.,  
RA Blemond C., Skali Z., Cattelico L., Poulain J., De Bernardis V.,  
RA Cnaud C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,  
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Wolff JN., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype."  
RL Nature 431:946-957(2004).  
RN [2]

RP NUCLEOTIDE SEQUENCE.  
RG Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
RL -!- CAUTION: The sequence shown here is derived from an

EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC Preliminary data.  
DR EMBL; CA601002358; CA67407.1; -, Genomic\_DNA.  
DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca\_bd.  
DR InterPro; IPR001438; EGF\_II.  
DR InterPro; IPR006209; EGF\_like.  
DR Pfam; PF00008; EGF\_1.  
DR PRINTS; PR00010; EGFBL00D.  
DR SMART; SM00179; EGF\_CA; 2.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 2.



```

DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 2.
DR EGF-like domain.
FT NON_TER 59
SQ SEQUENCE 59 AA; 6207 MW; 6BD9E51E9CA7F351 CRC64;

Query Match 18.0%; Score 61.5; DB 2; Length 59;
Best Local Similarity 37.5%; Pred. No. 11;
Matches 12; Conservative 3; Mismatches 12; Indels 5; Gaps 1;

OY 14 CVNGGECFVMDLSPSRYLCKPNEFTGDRCC 45
DB 4 CANGATC-----LQGVNRFSCVCPFGSGRRC 30

RESULT 11
OS IECA HUMAN
ID OSIECA_HUMAN PRELIMINARY; PRT; 57 AA.
AC OSIECA;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DE Nectin G1 isoform G11 (Fragment).
GN Name=NTNG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Meerbach J.M.A., Ohba H., Fukasawa M., Aoki M., Yoshikawa T.;
RT "Human nectin G1 isoforms show evidence of differential expression.";
RL Submitted (SEP-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY764264; AAM47411.1; -, mRNA.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR006210; IEGF.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS50026; EGF_3; 1.
FT NON_TER 1
FT NON_TER 57
SQ SEQUENCE 57 AA; 5983 MW; 74C6F2B66FB8475E CRC64;

Query Match 17.3%; Score 59; DB 2; Length 57;
Best Local Similarity 30.8%; Pred. No. 21;
Matches 12; Conservative 4; Mismatches 15; Indels 8; Gaps 1;

OY 8 EKEKTFVNGGECFVMDLSPSRYLCKPNEFTGDRCC 46
DB 14 DNEHLHCNGGTC-----NNVRCICPAAYTIGICE 44

RESULT 12
OS ICA TETNG
ID OSICA_TETNG PRELIMINARY; PRT; 44 AA.
AC OSICA;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Chromosome 5 SCAF14581, whole genome shotgun sequence.
DE (Fragment).
GN ORNames=GSTENG00017665001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OC NCBI_TaxID=998083;
RN [1]

```

```

RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costez C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anchaoud V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cartolico L., Poulain J., De Bernardis V.,
RA Craud C., Duprat S., Brotier P., Coutanceau J.P., Guzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.V., McEwan P., Boeak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Landet V., Schachter V., Querier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Croliis H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CA80104581; CAP99538.1; -, Genomic_DNA.
DR InterPro; IPR000152; Aax_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001438; EGF_Ca_bd.
DR InterPro; IPR001438; EGF_1.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00008; EGF; 1.
DR PRINTS; PR00010; EGFBLDOD.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00179; EGF_CA; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
KV EGF-like domain.
FT NON_TER 1
FT NON_TER 44
SQ SEQUENCE 44 AA; 4609 MW; 5A1DB8F7089FAC67 CRC64;

Query Match 17.1%; Score 58.5; DB 2; Length 44;
Best Local Similarity 30.3%; Pred. No. 19;
Matches 10; Conservative 7; Mismatches 11; Indels 5; Gaps 1;

OY 14 CVNGGECFVMDLSPSRYLCKPNEFTGDRCC 46
DB 10 CLNGGTC-----VDEVNQFSCVCSKSGSGPCCQ 37

RESULT 13
OS MZF7 BOVIN
ID OSMZF7_BOVIN PRELIMINARY; PRT; 39 AA.
AC OSMZF7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Tissue plasminogen activator (Fragment).
GN Name=PLAT;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20380829; PubMed=10920240; DOI=10.1007/s003350010130;
RA Sonstegard T.S., Garrett W.M., Ashwell M.S., Bennett G.L.,
RA Kappes S.M., Van Tassel C.P.;
RT "Comparative map alignment of BTA27 and HSA4 and 8 to identify

```

```

RT  conserved segments of genome containing fat deposition QTL."
RL  Mamm. Genome 11:682-688(2000). Genomic_DNA.
DR  EMBL; AF230195; AAF79125.1; -.
DR  HSSP; P00750; ITPG.
DR  InterPro; IPR000742; EGF_2.
DR  InterPro; IPR006209; EGF_like.
DR  InterPro; IPR000001; Kringle.
DR  Pfam; PF00051; Kringle; 1.
DR  PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR  PROSITE; PS01186; EGF_2; 1.
DR  PROSITE; PS50026; EGF_3; 1.
DR  Kringle.
KM  Kringle.
FT  NON_TER 1 1
FT  NON_TER 39 39
SQ  SEQUENCE 39 AA; 4236 MW; BDB3A28B38A67BCB CRC64;

Query Match 16.1%; Score 55; DB 2; Length 39;
Best Local Similarity 37.5%; Pred. No. 43;
Matches 9; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 32 YLCKCPNEFTGDRCONVMA5FYK 55
Db 2 FVCCPEGFWMKLCIEDATATCYK 25

RESULT 14
ID Q84KT0_BRAOL PRELIMINARY; PRT; 61 AA.
AC Q84KT0;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE S-locus protein 11 (Fragment).
GN Names=SP11-64;
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
ON 11;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=2286392; PubMed=12399400;
RA Sato K., Nishio T., Kimura R., Kusaba M., Suzuki T., Hatakeyama K.,
RT "Coevolution of the S-locus genes SRK, SLG and SP11/SCR in Brassica
RT oleracea and B. rapa."
RL Genetics 162:931-940(2002).
DR EMBL; AB054751; BAC24085.1; -. mRNA.
DR InterPro; IPR006209; EGF_like.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
FT NON_TER 1 1
FT NON_TER 61 AA; 6749 MW; 0744977FB9C07B34 CRC64;
SQ SEQUENCE 61 AA; 6749 MW; 0744977FB9C07B34 CRC64;

Query Match 16.1%; Score 55; DB 2; Length 61;
Best Local Similarity 50.0%; Pred. No. 67;
Matches 11; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

QY 29 PSRYLCKPNEFTGDRCONVYM 50
Db 41 PSK--CKCSNBSDGRCVCVLI 60

RESULT 15
ID Q9TX97_CAEEL PRELIMINARY; PRT; 52 AA.
AC Q9TX97;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE GLP-1 protein (Fragment).
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.

```

```

OX NCBI_TaxID=6239;
RN 11;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=93091267; PubMed=1457827;
RA Kodoyianni V., Maine E.M., Kimble J.;
RT "Molecular basis of loss-of-function mutations in the glp-1 gene of
RT Caenorhabditis elegans."
RL Mol. Biol. Cell 3:1199-1213(1992).
DR InterPro; IPR006209; EGF_like.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
SQ SEQUENCE 52 AA; 5782 MW; E56E1F31B64A0859 CRC64;

Query Match 15.6%; Score 53.5; DB 2; Length 52;
Best Local Similarity 26.8%; Pred. No. 87;
Matches 11; Conservative 6; Mismatches 15; Indels 9; Gaps 2;

QY 6 CAEKEKTCVNGGECFPMVDLSNPSRYLCKCPNEFTGDRQ 46
Db 21 CSRSNGTY-YNDRCI1-----NGFCVCEPDYIGDRCE 52

```

Search completed: January 26, 2006, 12:43:29  
Job time : 69 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 26, 2006, 12:40:22 ; Search time 23 Seconds

(without alignments)  
219.270 Million cell updates/sec

Title: US-09-980-672-2

Perfect score: 342  
Sequence: 1 SHLVKAEKKEKTCVNGGEC.....GDRCONYVNASFYKAEELY 61

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 323677

Minimum DB seq length: 0  
Maximum DB seq length: 61

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/aa/5 COMB.pep:\*
- 2: /cgn2\_6/prodata/1/aa/6 COMB.pep:\*
- 3: /cgn2\_6/prodata/1/aa/H COMB.pep:\*
- 4: /cgn2\_6/prodata/1/aa/PC/US COMB.pep:\*
- 5: /cgn2\_6/prodata/1/aa/RE COMB.pep:\*
- 6: /cgn2\_6/prodata/1/aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	337	98.5	60	2	US-08-341-018-64 Sequence 64, App1
2	337	98.5	60	2	US-08-470-335-222 Sequence 222, App
3	337	98.5	60	2	US-08-470-339-222 Sequence 222, App
4	337	98.5	60	2	US-08-467-602-416 Sequence 416, App
5	337	98.5	60	2	US-08-411-295F-99 Sequence 57, App1
6	337	98.5	60	2	US-08-411-295F-99 Sequence 57, App1
7	298	87.1	56	2	US-09-020-880-102 Sequence 102, App
8	298	87.1	56	2	US-09-101-544-102 Sequence 102, App
9	294	86.0	52	1	US-08-417-640A-2 Sequence 2, App1
10	294	86.0	52	1	US-08-760-815-2 Sequence 2, App1
11	294	86.0	52	1	US-08-761-038-2 Sequence 2, App1
12	294	86.0	52	2	US-09-020-880-92 Sequence 92, App1
13	294	86.0	52	2	US-09-101-544-92 Sequence 92, App1
14	294	86.0	53	2	US-09-097-681-18 Sequence 18, App1
15	294	86.0	54	1	US-08-179-481-112 Sequence 112, App
16	293	85.7	56	2	US-09-020-880-101 Sequence 101, App
17	293	85.7	56	2	US-09-101-544-101 Sequence 101, App
18	287	83.9	50	1	US-08-036-5558-151 Sequence 151, App
19	287	83.9	50	1	US-08-469-569-151 Sequence 151, App
20	287	83.9	50	1	US-08-249-322A-151 Sequence 151, App
21	287	83.9	50	1	US-08-469-526A-151 Sequence 151, App
22	287	83.9	50	1	US-08-734-591A-151 Sequence 151, App
23	287	83.9	50	1	US-08-469-660-151 Sequence 151, App
24	287	83.9	50	2	US-08-470-335-151 Sequence 151, App
25	287	83.9	50	2	US-08-735-021-151 Sequence 151, App
26	287	83.9	50	2	US-08-735-021-190 Sequence 190, App
27	287	83.9	50	2	US-08-734-664A-151 Sequence 151, App

28	287	83.9	50	2	US-08-470-339-151 Sequence 151, App
29	287	83.9	50	2	US-08-467-602-151 Sequence 151, App
30	287	83.9	50	4	PCT-US94-05083C-147 Sequence 147, App
31	287	83.9	50	4	PCT-US95-06846A-151 Sequence 151, App
32	287	83.9	56	2	US-09-020-880-111 Sequence 111, App
33	287	83.9	56	2	US-09-101-544-111 Sequence 111, App
34	286	83.6	50	2	US-08-753-007A-14 Sequence 14, App1
35	286	83.6	50	2	US-09-398-496-14 Sequence 14, App1
36	282	82.5	56	2	US-09-020-880-96 Sequence 96, App1
37	282	82.5	56	2	US-09-101-544-96 Sequence 96, App1
38	279	81.6	56	2	US-09-020-880-108 Sequence 108, App
39	279	81.6	56	2	US-09-101-544-108 Sequence 108, App
40	277	81.0	48	2	US-08-899-437-15 Sequence 15, App1
41	277	81.0	48	2	US-09-126-121-15 Sequence 15, App1
42	276	80.7	56	2	US-09-020-880-97 Sequence 97, App1
43	276	80.7	56	2	US-09-020-880-99 Sequence 99, App1
44	276	80.7	56	2	US-09-101-544-97 Sequence 97, App1
45	276	80.7	56	2	US-09-101-544-99 Sequence 99, App1

#### ALIGNMENTS

```
RESULT 1
US-08-341-018-64
; Sequence 64, Application US/08341018A
; Patent No. 6087323
; GENERAL INFORMATION:
; APPLICANT: Gwynne, David I.
; APPLICANT: Mahanthappa, Nagesh K.
; APPLICANT: Marchionni, Mark A.
; APPLICANT: Birmingham-McDonogh, Olivia
; APPLICANT: McBurney, Robert N.
; TITLE OF INVENTION: USE OF NEUREGULINS AS MODULATORS OF
; FILE REFERENCE: 04585/041001
; CURRENT APPLICATION NUMBER: US/08/341,018A
; CURRENT FILING DATE: 1994-11-17
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-341-018-64

Query Match      98.5%: Score 337; DB 2; Length 60;
Best Local Similarity 100.0%: Pred. No. 9.1e-33;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SHLVKAEKKEKTCVNGGECFMVKDLSNPSRYLCKCFNEFTGDRCONYVNASFYKAEELY 60
DB      1 SHLVKAEKKEKTCVNGGECFMVKDLSNPSRYLCKCFNEFTGDRCONYVNASFYKAEELY 60

RESULT 2
US-08-470-335-222
; Sequence 222, Application US/08470335F
; Patent No. 6147190
; GENERAL INFORMATION:
; APPLICANT: GOODERL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHERTTI, LOUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; FILE REFERENCE: 04585/00200B
; CURRENT APPLICATION NUMBER: US/08/470,335F
; CURRENT FILING DATE: 1995-06-06
```

```

? EARLIER APPLICATION NUMBER: 08/036,555
? EARLIER FILING DATE: 1993-03-24
? NUMBER OF SEQ ID NOS: 252
? SOFTWARE: PASTSEQ for Windows Version 4.0
? SEQ ID NO 222
? LENGTH: 60
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-08-470-335-222

```

Query Match	98.5%	Score 337	DB 2	Length 60
Best Local Similarity	100.0%	Pred. No. 9.1e-33		
Matches 60	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy 1 SHLVKAEKEKTFVNGSGECFWMVKDLSNSRRLCKCPNETGDRCONYVMA SFYKAEELY 60

Db 1 SHLVKAEKEKTFVNGSGECFWMVKDLSNSRRLCKCPNETGDRCONYVMA SFYKAEELY 60

RESULT 3  
US-08-470-339-222  
; Sequence 222, Application US/08470339C

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-470-339-222

```

Qy 1 SHLVKAEKEKTECVNGGECFMVXKDSLNSPARYLKCPNEFTGDRCONYVMA SFYKAEELY 600

Db 1 SHLVKAEKEKTEPCVNGGECFMVXKDSLNSPARYLKCPNEFTGDRCONYVMA SFYKAEELY 600

```

RESULT 4
US-08-467-602-416
; Sequence 416, Application US/08467602C
; Patent No. 644642
; GENERAL INFORMATION:
; APPLICANT: Schlar, Robert
; APPLICANT: Markiomli, Mark
; APPLICANT: Gayme, David I.
; TITLE OF INVENTION: METHODS FOR TREATING MUSCLE DISEASES AND
; TITLE OF INVENTION: DISORDERS

```

```

? FILE REFERENCE: 04585\028003
? CURRENT APPLICATION NUMBER: US/08/467,602C
? FILING DATE: 1995-06-06
? EARLIER APPLICATION NUMBER: 08/209,204
? EARLIER FILING DATE: 1994-03-08
? EARLIER APPLICATION NUMBER: 08/059,022
? EARLIER FILING DATE: 1993-05-06
? NUMBER OF SEQ ID NOS: 420
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 416
? LENGTH: 60
? TYPE: PR1
? ORGANISM: Homo sapiens
? US-08-467-602-416

```

Query Match	98.5%	Score 337	DB 2	Length 60
Best Local Similarity	100.0%	Pred. No. 9.1e-33		
Matches 60	Conservative 0	Mismatches 0	Indels	

Qy 1 SHLVKAEKEKTF CVANGGECF MWKDL SNPSRYLCKPNEFTGDRCONYYMAASFYKAEELY 60

Db 1 SHLVKAEKEKTF CVANGGECF MWKDL SNPSRYLCKPNEFTGDRCONYYMAASFYKAEELY 60

```

RESULT 5
US-08-411-295F-57
; Sequence 57, Application US/08411295F
; Patent No. 6750196
; GENERAL INFORMATION:
; APPLICANT: REH, THOMAS A.
; APPLICANT: MARCHIONNI, MARK A.
; APPLICANT: MCCABE, KATHYRN L.
; APPLICANT: BIRMINGHAM-MCDONOUGH, OLIVIA
; APPLICANT: MAHANTHAPPA, NAGESH K.
; APPLICANT: GWYNNE, DAVID I.
; TITLE OF INVENTION: Methods of Treating Disorders of the Eye
; FILE REFERENCE: 04585/039001
; CURRENT APPLICATION NUMBER: US/08/411,295F
; CURRENT FILING DATE: 1995-03-27
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: SeqSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 60
; TYPE: prt
; ORGANISM: Homo sapiens
US-08-411-295F-57

```

Query Match	98.5%	Score 3377	DB 2	Length 60
Best Local Similarity	100.0%	Pred. No. 9.1e-33		
Matches 60	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy 1 SHLVKAEKEKTFVNGGECFPMWKDLSNPSRYLCKCPNETGTDRCONYVMAFYKAEELY 66

Db 1 SHLVKAEKEKTFVNGGECFPMWKDLSNPSRYLCKCPNETGTDRCONYVMAFYKAEELY 66

```

RESULT 6
US-08-411-295F-99
; Sequence 99, Application US/08411295F
; Patent No. 6750196
; GENERAL INFORMATION:
; APPLICANT: REH, THOMAS A.
; APPLICANT: MARCIONNI, MARK A.
; APPLICANT: MCCABE, KATHYRN L.
; APPLICANT: BERMINGHAM-MCDONOUGH, OLIVIA
; APPLICANT: MAHANTHAPPA, NAGESH K.
; APPLICANT: GWYNNE, DAVID I.
; TITLE OF INVENTION: Methods of Treating Disorders of the Eye
; FILE REFERENCE: 04585/039001
; CURRENT APPLICATION NUMBER: US/08/411,295F
; CURRENT FILING DATE: 1995-03-27
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: FastSeq for Windows Version 4.0

```

SEQ ID NO 99  
 LENGTH: 60  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-08-411-295F-99

Query Match 98.5%; Score 337; DB 2; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-33;  
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLVKAEKKEKTCVNGGECFMVVDLSNPSRYLCKCPNEFTGDRCONVYMASFY 60  
 DB 1 SHLVKAEKKEKTCVNGGECFMVVDLSNPSRYLCKCPNEFTGDRCONVYMASFYKAEELY 60

RESULT 7  
 US-09-020-880-102  
 Sequence 102, Application US/09020880A  
 Patent No. 6136558  
 GENERAL INFORMATION:  
 APPLICANT: Genentech, Inc.  
 APPLICANT: Ballinger, Marcus D.  
 APPLICANT: Jones, Jennifer T.  
 APPLICANT: Fairbrother, Wayne J.  
 APPLICANT: Sliwowski, Mark X.  
 APPLICANT: Wells, James A.  
 TITLE OF INVENTION: HERGULIN VARIANTS  
 FILE REFERENCE: 14918-720CON1  
 CURRENT APPLICATION NUMBER: US/09/020, 880A  
 CURRENT FILING DATE: 1998-02-09  
 EARLIER APPLICATION NUMBER: US 60/037,581  
 EARLIER FILING DATE: 1997-02-10  
 NUMBER OF SEQ ID NOS: 116  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 102  
 LENGTH: 56  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-020-880-102

Query Match 87.1%; Score 298; DB 2; Length 56;  
 Best Local Similarity 96.3%; Pred. No. 3.4e-28;  
 Matches 52; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLVKAEKKEKTCVNGGECFMVVDLSNPSRYLCKCPNEFTGDRCONVYMASFY 54  
 DB 3 SHLVKAEKKEKTCVNGGECFMVVDLSNPSRYLCKCPNEFTGDRCONVYMASFY 56

RESULT 8  
 US-09-101-544-102  
 Sequence 102, Application US/09101544  
 Patent No. 6387638  
 GENERAL INFORMATION:  
 APPLICANT: Genentech, Inc.  
 APPLICANT: Ballinger, Marcus D.  
 APPLICANT: Jones, Jennifer T.  
 APPLICANT: Fairbrother, Wayne J.  
 APPLICANT: Sliwowski, Mark X.  
 APPLICANT: Wells, James A.  
 TITLE OF INVENTION: HERGULIN VARIANTS  
 FILE REFERENCE: 14918-720CON2  
 CURRENT APPLICATION NUMBER: US/09/101,544  
 CURRENT FILING DATE: 1998-07-17  
 PRIOR APPLICATION NUMBER: US 09/020,880  
 PRIOR FILING DATE: 1998-02-09  
 PRIOR APPLICATION NUMBER: US 60/037,581  
 PRIOR FILING DATE: 1997-02-10  
 NUMBER OF SEQ ID NOS: 116  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 102  
 LENGTH: 56  
 TYPE: PRT

ORGANISM: Homo sapiens  
 US-09-101-544-102

Query Match 87.1%; Score 298; DB 2; Length 56;  
 Best Local Similarity 96.3%; Pred. No. 3.4e-28;  
 Matches 52; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SHLVKAEKKEKTCVNGGECFMVVDLSNPSRYLCKCPNEFTGDRCONVYMASFY 54  
 DB 3 SHLVKAEKKEKTCVNGGECFMVVDLSNPSRYLCKCPNEFTGDRCONVYMASFY 56

RESULT 9  
 US-08-417-640A-2  
 Sequence 2, Application US/08417640A  
 Patent No. 5670342  
 GENERAL INFORMATION:  
 APPLICANT: Carnahan, Josette F.  
 APPLICANT: Hara, Shinichi  
 APPLICANT: Lu, Hsieng S.  
 APPLICANT: Mayer, John P.  
 APPLICANT: Yoshinaga, Steven K.  
 TITLE OF INVENTION: NDF Peptides  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Amgen Inc.  
 STREET: 1840 Denavilland Drive  
 CITY: Thousand Oaks  
 STATE: California  
 COUNTRY: USA  
 ZIP: 91320

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/417,640A  
 FILING DATE:  
 CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:  
 NAME: Mazza, Richard J.  
 REFERENCE/DOCKET NUMBER: A-310  
 INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 52 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-417-640A-2

Query Match 86.0%; Score 294; DB 1; Length 52;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-28;  
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLVKAEKKEKTCVNGGECFMVVDLSNPSRYLCKCPNEFTGDRCONVYMASFY 52  
 DB 1 SHLVKAEKKEKTCVNGGECFMVVDLSNPSRYLCKCPNEFTGDRCONVYMASFY 52

RESULT 10  
 US-08-760-815-2  
 Sequence 2, Application US/08760815  
 Patent No. 5686415  
 GENERAL INFORMATION:  
 APPLICANT: Carnahan, Josette F.  
 APPLICANT: Hara, Shinichi  
 APPLICANT: Lu, Hsieng S.  
 APPLICANT: Mayer, John P.  
 APPLICANT: Yoshinaga, Steven K.  
 TITLE OF INVENTION: NDF Peptides  
 NUMBER OF SEQUENCES: 6

RESPONSE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/760,815  
FILING DATE: 05-DEC-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/417,640  
FILING DATE: 06-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Marza, Richard J.  
REFERENCE/DOCKET NUMBER: A-310  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 52 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-760-815-2

Query Match 86.0%; Score 294; DB 1; Length 52;  
Best Local Similarity 100.0%; Pred. No. 9.3e-28;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYMAS 52  
Db 1 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYMAS 52

RESULT 11  
US-08-761-038-2  
Sequence 2, Application US/08761038  
Patent No. 5929032  
GENERAL INFORMATION:  
APPLICANT: Carnahan, Josette F.  
APPLICANT: Hara, Shinichi  
APPLICANT: Lu, Hsiang S.  
APPLICANT: Mayer, John P.  
APPLICANT: Yoshinaga, Steven K.  
TITLE OF INVENTION: NDF Peptides  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/761,038  
FILING DATE: 05-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/417,640  
FILING DATE: 06-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Marza, Richard J.

REFERENCE/DOCKET NUMBER: A-310  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 52 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-761-038-2

Query Match 86.0%; Score 294; DB 1; Length 52;  
Best Local Similarity 100.0%; Pred. No. 9.3e-28;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYMAS 52  
Db 1 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYMAS 52

RESULT 12  
US-09-020-880-92  
Sequence 92, Application US/09020880A  
Patent No. 6136558  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ballinger, Marcus D.  
APPLICANT: Jones, Jennifer T.  
APPLICANT: Fairbrother, Wayne J.  
APPLICANT: Sliwkowski, Mark X.  
APPLICANT: Wells, James A.  
TITLE OF INVENTION: HERGULIN VARIANTS  
FILE REFERENCE: 14918-720CON1  
CURRENT APPLICATION NUMBER: US/09/020,880A  
CURRENT FILING DATE: 1998-02-09  
EARLIER APPLICATION NUMBER: US 60/037,581  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 92  
LENGTH: 52  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-020-880-92

Query Match 86.0%; Score 294; DB 2; Length 52;  
Best Local Similarity 100.0%; Pred. No. 9.3e-28;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYMAS 52  
Db 1 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYMAS 52

RESULT 13  
US-09-101-544-92  
Sequence 92, Application US/09101544  
Patent No. 6387638  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ballinger, Marcus D.  
APPLICANT: Jones, Jennifer T.  
APPLICANT: Fairbrother, Wayne J.  
APPLICANT: Sliwkowski, Mark X.  
APPLICANT: Wells, James A.  
TITLE OF INVENTION: HERGULIN VARIANTS  
FILE REFERENCE: 14918-720CON2  
CURRENT APPLICATION NUMBER: US/09/101,544  
CURRENT FILING DATE: 1998-07-17  
PRIOR APPLICATION NUMBER: US 09/020,880  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: US 60/037,581  
PRIOR FILING DATE: 1997-02-10  
NUMBER OF SEQ ID NOS: 116

SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 92  
LENGTH: 52  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-101-544-92

Query Match 86.0%; Score 294; DB 2; Length 52;  
Best Local Similarity 100.0%; Pred. No. 9.3e-28;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SHLVKAEKKEKTFVNGGECFVMDLSNPSRYLCKCPNEFTGDRCONVYMAS 52  
Db 1 SHLVKAEKKEKTFVNGGECFVMDLSNPSRYLCKCPNEFTGDRCONVYMAS 52

## RESULT 14

US-09-097-681-18  
Sequence 18, Application US/09097681  
Patent No. 6727077  
GENERAL INFORMATION:  
APPLICANT: Young, Paul  
APPLICANT: King, C. Richter  
APPLICANT: Hlazi, Mai  
APPLICANT: Ruben, Steve  
TITLE OF INVENTION: Heregulin-Like Factor  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/097,681  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/049,942  
FILING DATE: 17-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoover, Kenley K.  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PF383PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8439  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 53 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-097-681-18

Query Match 86.0%; Score 294; DB 2; Length 53;  
Best Local Similarity 100.0%; Pred. No. 9.5e-28;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SHLVKAEKKEKTFVNGGECFVMDLSNPSRYLCKCPNEFTGDRCONVYMAS 52  
Db 2 SHLVKAEKKEKTFVNGGECFVMDLSNPSRYLCKCPNEFTGDRCONVYMAS 53

RESULT 15  
US-08-179-481-112

Sequence 112, Application US/08179481  
Patent No. 5624816  
GENERAL INFORMATION:  
APPLICANT: CARRAWAY, KERMIT L.  
APPLICANT: CAROTHERS, CARRAWAY, CORALIE A.  
APPLICANT: FREGIEN, NEVIS L.  
TITLE OF INVENTION: ONCOGENE PRODUCT LIGAND  
NUMBER OF SEQUENCES: 125  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/179,481  
FILING DATE: 28-DEC-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/922,521  
FILING DATE: 30-JUL-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 200702/UM92-08CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEQ ID NO: 112:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 54 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-179-481-112

Query Match 86.0%; Score 294; DB 1; Length 54;  
Best Local Similarity 100.0%; Pred. No. 9.7e-28;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SHLVKAEKKEKTFVNGGECFVMDLSNPSRYLCKCPNEFTGDRCONVYMAS 52  
Db 3 SHLVKAEKKEKTFVNGGECFVMDLSNPSRYLCKCPNEFTGDRCONVYMAS 54

Search completed: January 26, 2006, 12:44:29  
Job time : 23 secs

**THIS PAGE BLANK (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 26, 2006, 12:43:33 ; Search time 113 Seconds  
(without alignments)  
225.554 Million cell updates/sec

Title: US-09-980-672-2

Perfect score: 342  
Sequence: 1 SHLVKCAEKETFCVNGSEC.....GDRCONYMASFYKAEELyq 61

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 620404

Minimum DB seq length: 0  
Maximum DB seq length: 61

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	300	87.7	53	US-10-485-683-13	Sequence 13, Appl
2	298	87.1	56	US-10-082-747A-102	Sequence 102, App
3	294	86.0	52	US-10-082-747A-92	Sequence 92, Appl
4	294	86.0	53	US-10-609-370-18	Sequence 18, Appl
5	293	85.7	56	US-10-082-747A-101	Sequence 101, App
6	287	83.9	50	US-08-736-019-151	Sequence 151, App
7	287	83.9	50	US-10-844-218-151	Sequence 151, App
8	287	83.9	56	US-10-082-747A-111	Sequence 111, App
9	286	83.6	50	US-10-082-241-14	Sequence 14, Appl
10	286	83.6	50	US-10-899-227-14	Sequence 14, Appl
11	282	82.5	56	US-10-082-747A-96	Sequence 96, Appl
12	279	81.6	56	US-10-082-747A-108	Sequence 108, App
13	277	81.0	48	US-09-817-647-15	Sequence 15, Appl
14	277	81.0	48	US-09-877-665-15	Sequence 15, Appl
15	277	81.0	48	US-10-136-573A-15	Sequence 15, Appl
16	277	81.0	48	US-10-215-862-15	Sequence 15, Appl
17	277	81.0	48	US-10-944-116-15	Sequence 15, Appl
18	277	81.0	48	US-11-035-787-15	Sequence 15, Appl
19	276	80.7	56	US-10-082-747A-97	Sequence 97, Appl
20	276	80.7	56	US-10-082-747A-99	Sequence 99, Appl
21	274	80.1	49	US-10-240-411-4	Sequence 4, Appl
22	274	80.1	52	US-10-082-747A-28	Sequence 28, Appl
23	272	79.5	56	US-10-082-747A-95	Sequence 95, Appl
24	272	79.5	56	US-10-082-747A-104	Sequence 104, App
25	271	79.2	56	US-10-082-747A-100	Sequence 100, App
26	270	78.9	56	US-10-082-747A-98	Sequence 98, Appl
27	269	78.7	56	US-10-082-747A-94	Sequence 94, Appl

28	268.5	78.5	49	US-10-082-747A-14	Sequence 14, Appl
29	267	78.1	56	US-10-082-747A-105	Sequence 105, App
30	266	77.8	52	US-10-082-747A-25	Sequence 25, Appl
31	264.5	77.3	49	US-10-082-747A-16	Sequence 16, Appl
32	263	76.9	56	US-10-082-747A-112	Sequence 112, App
33	260	76.0	56	US-10-082-747A-109	Sequence 109, App
34	256	74.9	56	US-10-082-747A-110	Sequence 110, App
35	254	74.3	52	US-10-082-747A-22	Sequence 22, Appl
36	252	73.7	56	US-10-082-747A-106	Sequence 106, App
37	251	73.4	56	US-10-082-747A-103	Sequence 103, App
38	251	73.4	56	US-10-082-747A-115	Sequence 115, App
39	250	73.1	52	US-10-082-747A-29	Sequence 29, Appl
40	248	72.5	56	US-10-082-747A-113	Sequence 113, App
41	244	71.3	50	US-10-082-241-15	Sequence 15, Appl
42	244	71.3	50	US-10-899-227-15	Sequence 15, Appl
43	238	69.6	52	US-10-082-747A-17	Sequence 17, Appl
44	236.5	69.2	49	US-10-082-747A-21	Sequence 21, Appl
45	236	69.0	56	US-10-082-747A-107	Sequence 107, App

# ALIGNMENTS

RESULT 1  
US-10-485-683-13  
Sequence 13, Application US/10485683  
Publication No. US20040248196A1  
GENERAL INFORMATION:  
APPLICANT: ADAMS, TIMOTHY EDWARD  
APPLICANT: BURGESS, ANTONY WILKS  
APPLICANT: EILEMAN, THOMAS CHARLES  
APPLICANT: GARRETT, THOMAS PETER JOHN  
APPLICANT: JORISSEN, ROBERT NICHOLAS  
APPLICANT: LOU, MEIZHEN  
APPLICANT: LOVREZ, GEORGE OSCAR  
APPLICANT: MCKERN, NEIL MORETON  
APPLICANT: NICE, EDOUARD COLLINS  
APPLICANT: WARD, COLIN WESLEY  
TITLE OF INVENTION: METHODS OF SCREENING BASED ON THE EGF RECEPTOR CRYSTAL  
FILE REFERENCE: 051654/0104  
CURRENT APPLICATION NUMBER: US/10/485,683  
CURRENT FILING DATE: 2004-02-03  
PRIOR APPLICATION NUMBER: PCT/AU02/01042  
PRIOR FILING DATE: 2002-08-05  
PRIOR APPLICATION NUMBER: AU PR 6827  
PRIOR FILING DATE: 2001-08-03  
PRIOR APPLICATION NUMBER: AU PR 6828  
PRIOR FILING DATE: 2001-08-03  
PRIOR APPLICATION NUMBER: 60/336,560  
PRIOR FILING DATE: 2001-11-01  
PRIOR APPLICATION NUMBER: 60/335,393  
PRIOR FILING DATE: 2001-11-01  
PRIOR APPLICATION NUMBER: AU PS 2731  
PRIOR FILING DATE: 2002-05-31  
PRIOR APPLICATION NUMBER: 60/388,171  
PRIOR FILING DATE: 2002-06-11  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 13  
LENGTH: 53  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-485-683-13

Query Match 87.7%; Score 300; DB 5; Length 53;  
Best Local Similarity 100.0%; Pred. No. 9.9e-28;  
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SHLVKCAEKETFCVNGSECFMVYDLSNPSRYLCKPNEFTGDRCONYMASF 53  
1 SHLVKCAEKETFCVNGSECFMVYDLSNPSRYLCKPNEFTGDRCONYMASF 53

```
RESULT 2
US-10-082-747A-102
/ Sequence 102, Application US/10082747A
/ Publication No. US20030129688A1
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ APPLICANT: Ballinger, Marcus D.
/ APPLICANT: Jones, Jennifer T.
/ APPLICANT: Fairbrother, Wayne J.
/ APPLICANT: Sliwkowski, Mark X.
/ APPLICANT: Wells, James A.
/ TITLE OF INVENTION: HERGULIN VARIANTS
/ FILE REFERENCE: 402E-476112US
/ CURRENT APPLICATION NUMBER: US/10/082,747A
/ PRIOR FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: US 09/101,544
/ PRIOR FILING DATE: 1998-07-17
/ PRIOR APPLICATION NUMBER: PCT/US/98/01579
/ PRIOR FILING DATE: 1998-02-10
/ PRIOR APPLICATION NUMBER: US 08/799,054
/ PRIOR FILING DATE: 1997-02-10
/ NUMBER OF SEQ ID NOS: 116
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 102
/ LENGTH: 56
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-082-747A-102
```

```
Query Match      87.1%; Score 298; DB 4; Length 56;
Best Local Similarity 96.3%; Pred. No. 1.8e-27;
Matches 52; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 SHLVKAEKERTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMASFY 54  
|||||

DB 3 SHLVKAEKERTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMASFY 56  
|||||

```
RESULT 3
US-10-082-747A-92
/ Sequence 92, Application US/10082747A
/ Publication No. US20030129688A1
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ APPLICANT: Ballinger, Marcus D.
/ APPLICANT: Jones, Jennifer T.
/ APPLICANT: Fairbrother, Wayne J.
/ APPLICANT: Sliwkowski, Mark X.
/ APPLICANT: Wells, James A.
/ TITLE OF INVENTION: HERGULIN VARIANTS
/ FILE REFERENCE: 402E-476112US
/ CURRENT APPLICATION NUMBER: US/10/082,747A
/ PRIOR FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: US 09/101,544
/ PRIOR FILING DATE: 1998-07-17
/ PRIOR APPLICATION NUMBER: PCT/US/98/01579
/ PRIOR FILING DATE: 1998-02-10
/ PRIOR APPLICATION NUMBER: US 08/799,054
/ PRIOR FILING DATE: 1997-02-10
/ NUMBER OF SEQ ID NOS: 116
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 92
/ LENGTH: 52
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-082-747A-92
```

Query Match 86.0%; Score 294; DB 4; Length 52;  
Best Local Similarity 100.0%; Pred. No. 4.9e-27;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLVKAEKERTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMAS 52

```
Db 1 SHLVKAEKERTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMAS 52  
|||||
```

RESULT 4  
US-10-609-370-18  
/ Sequence 18, Application US/10609370  
/ Publication No. US20040048295A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Young et al.  
/ TITLE OF INVENTION: Heregulin-Like Factor  
/ FILE REFERENCE: PF383D1  
/ CURRENT APPLICATION NUMBER: US/10/609,370  
/ PRIOR FILING DATE: 2003-07-01  
/ PRIOR APPLICATION NUMBER: 09/097,681  
/ PRIOR FILING DATE: 1998-06-16  
/ PRIOR APPLICATION NUMBER: 60/049,942  
/ PRIOR FILING DATE: 1997-06-17  
/ NUMBER OF SEQ ID NOS: 22  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO 18  
/ LENGTH: 53  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-609-370-18

Query Match 86.0%; Score 294; DB 4; Length 53;  
Best Local Similarity 100.0%; Pred. No. 5e-27;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SHLVKAEKERTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMAS 52  
|||||

DB 2 SHLVKAEKERTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMAS 53  
|||||

```
RESULT 5
US-10-082-747A-101
/ Sequence 101, Application US/10082747A
/ Publication No. US20030129688A1
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ APPLICANT: Ballinger, Marcus D.
/ APPLICANT: Jones, Jennifer T.
/ APPLICANT: Fairbrother, Wayne J.
/ APPLICANT: Sliwkowski, Mark X.
/ APPLICANT: Wells, James A.
/ TITLE OF INVENTION: HERGULIN VARIANTS
/ FILE REFERENCE: 402E-476112US
/ CURRENT APPLICATION NUMBER: US/10/082,747A
/ PRIOR FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: US 09/101,544
/ PRIOR FILING DATE: 1998-07-17
/ PRIOR APPLICATION NUMBER: PCT/US/98/01579
/ PRIOR FILING DATE: 1998-02-10
/ PRIOR APPLICATION NUMBER: US 08/799,054
/ PRIOR FILING DATE: 1997-02-10
/ NUMBER OF SEQ ID NOS: 116
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 101
/ LENGTH: 56
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-082-747A-101
```

Query Match 85.7%; Score 293; DB 4; Length 56;  
Best Local Similarity 96.3%; Pred. No. 7e-27;  
Matches 52; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SHLVKAEKERTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMASFY 54  
|||||

DB 3 SHLVKAEKERTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMASFY 56  
|||||

RESULT 6  
US-08-736-019-151  
; Sequence 151, Application US/08736019  
; Publication No. US20030207799A1  
; GENERAL INFORMATION:  
; APPLICANT: Goodearl, Andrew  
; APPLICANT: Stroobant, Paul  
; APPLICANT: Minghetti, Luisa  
; APPLICANT: Waterfield, Michael  
; APPLICANT: Marchionni, Mark  
; APPLICANT: Chen, Mario  
; APPLICANT: Hiles, Ian  
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR  
; PREPARATION AND USE  
; NUMBER OF SEQUENCES: 189  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Clark & Ebling LLP  
; STREET: 176 Federal Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM Compatible Pentium  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/736, 019  
; FILING DATE: 22-OCT-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/471, 833  
; FILING DATE: 06-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/036, 555  
; FILING DATE: 24-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/965, 173  
; FILING DATE: 23-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/907, 138  
; FILING DATE: 30-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/940, 389  
; FILING DATE: 03-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/863, 703  
; FILING DATE: 03-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: UK 91 07566.3  
; FILING DATE: 10-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bleker-Brady, Kristina  
; REGISTRATION NUMBER: 39,109  
; REFERENCE/DOCKET NUMBER: 04585/00200Q  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 428-0200  
; TELEFAX: (617) 428-7045  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 151:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; US-08-736-019-151

Query Match 83.9%; Score 287; DB 2; Length 50;  
Best Local Similarity 100.0%; Pred. No. 3,1e-26;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 KCAKEKTFVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMASFY 54

DB 1 KCAKEKTFVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMASFY 50

RESULT 7  
US-10-844-218-151  
; Sequence 151, Application US/10844218  
; Publication No. US20050106666A1  
; GENERAL INFORMATION:  
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;  
; Minghetti, Luisa; Waterfield, Michael; Marchionni, Mark;  
; Chen, Mario; Su; Hiles, Ian  
; TITLE OF INVENTION: Glial Mitogenic Factors, Their  
; Preparation and Use  
; NUMBER OF SEQUENCES: 184  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felte & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York City  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
; COMPUTER: IBM  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/844, 218  
; FILING DATE: 12-AUG-2004  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/036, 555  
; FILING DATE: 24-MAR-1993  
; APPLICATION NUMBER: 07/965, 173  
; FILING DATE: 23-OCT-1992  
; APPLICATION NUMBER: 07/940, 389  
; FILING DATE: 03-SEP-1992  
; APPLICATION NUMBER: 07/907, 138  
; FILING DATE: 30-JUN-1992  
; APPLICATION NUMBER: 07/863, 703  
; FILING DATE: 03-APRIL-1992  
; APPLICATION NUMBER: U.K. 91 07566.3  
; FILING DATE: 10-APRIL-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Tsai, Christine H.  
; REGISTRATION NUMBER: 34,266  
; REFERENCE/DOCKET NUMBER: LUD 5250.4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884  
; INFORMATION FOR SEQ ID NO: 151:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50  
; TYPE: amino acid  
; STRANDEDNESS: <unknown>  
; TOPOLOGY: linear  
; US-10-844-218-151

Query Match 83.9%; Score 287; DB 5; Length 50;  
Best Local Similarity 100.0%; Pred. No. 3,1e-26;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 KCAKEKTFVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMASFY 54

DB 1 KCAKEKTFVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYMASFY 50

RESULT 8  
US-10-082-747A-111  
; Sequence 111, Application US/10082747A  
; Publication No. US20030129688A1

```
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ APPLICANT: Ballinger, Marcus D.
/ APPLICANT: Jones, Jennifer T.
/ APPLICANT: Fairbrother, Wayne J.
/ APPLICANT: Sliwkowski, Mark X.
/ APPLICANT: Wells, James A.
/ TITLE OF INVENTION: HEREGULIN VARIANTS
/ FILE REFERENCE: 402E-476112US
/ CURRENT APPLICATION NUMBER: US/10/082,747A
/ PRIOR FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: US 09/101,544
/ PRIOR FILING DATE: 1998-07-17
/ PRIOR APPLICATION NUMBER: PCT/US/98/01579
/ PRIOR FILING DATE: 1998-02-10
/ PRIOR APPLICATION NUMBER: US 08/799,054
/ PRIOR FILING DATE: 1997-02-10
/ NUMBER OF SEQ ID NOS: 116
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 111
/ LENGTH: 56
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-082-747A-111

Query Match      83.9%; Score 287; DB 4; Length 56;
Best Local Similarity 92.6%; Pred. No. 3,5e-26;
Matches 50; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy      1 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYMASFY 54
Db      3 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYMASFY 56

RESULT 9
US-10-096-241-14
/ Sequence 14, Application US/10096241
/ Publication No. US20020127594A1
/ GENERAL INFORMATION:
/ APPLICANT: Gearing, David P.
/ TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
/ AND USES THEREFOR
/ NUMBER OF SEQUENCES: 33
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson P.C.
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: US
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/096,241
/ FILING DATE: 12-Mar-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/699,591
/ FILING DATE: 19-AUG-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fasse, J. Peter
/ REGISTRATION NUMBER: 32,983
/ REFERENCE/DOCKET NUMBER: 07334/022001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-542-5070
/ TELEFAX: 617-542-8906
/ TELEX: <Unknown>
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
```

```
/ LENGTH: 50 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-096-241-14

Query Match      83.6%; Score 286; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.1e-26;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYM 50
Db      1 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYM 50

RESULT 10
US-10-899-227-14
/ Sequence 14, Application US/10899227
/ Publication No. US20040265970A1
/ GENERAL INFORMATION:
/ APPLICANT: Gearing, David P.
/ TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
/ AND USES THEREFOR
/ NUMBER OF SEQUENCES: 33
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson P.C.
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: US
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/899,227
/ FILING DATE: 26-Jul-2004
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/10/096,241
/ FILING DATE: 12-Mar-2002
/ APPLICATION NUMBER: 08/699,591
/ FILING DATE: 19-AUG-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fasse, J. Peter
/ REGISTRATION NUMBER: 32,983
/ REFERENCE/DOCKET NUMBER: 07334/022001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-542-5070
/ TELEFAX: 617-542-8906
/ TELEX: <Unknown>
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 50 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-899-227-14

Query Match      83.6%; Score 286; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.1e-26;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYM 50
Db      1 SHLVKCAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONVYM 50
```

RESULT 11  
US-10-082-747A-96

; Sequence 96, Application US/10082747A  
; Publication No. US20030129688A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ballinger, Marcus D.  
; APPLICANT: Jones, Jennifer T.  
; APPLICANT: Fairbrother, Wayne J.  
; APPLICANT: Sliwkowski, Mark X.  
; APPLICANT: Wells, James A.  
; TITLE OF INVENTION: HERGULIN VARIANTS  
; FILE REFERENCE: 402E-476112US  
; CURRENT APPLICATION NUMBER: US/10/082,747A  
; PRIOR FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: US 09/101,544  
; PRIOR FILING DATE: 1998-07-17  
; PRIOR APPLICATION NUMBER: PCT/US/98/01579  
; PRIOR FILING DATE: 1998-02-10  
; PRIOR APPLICATION NUMBER: US 08/799,054  
; PRIOR FILING DATE: 1997-02-10  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 96  
; LENGTH: 56  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-082-747A-96

Query Match 82.5%; Score 282; DB 4; Length 56;  
Best Local Similarity 90.7%; Pred. No. 1.4e-25;  
Matches 49; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SHLVKCAEKEKTFVNGGECFVMDLSNPSRYLCKCPNEFTGDRCONVYMASFY 54  
Db 3 SHLVKCAEKEKTFVNGGECFVMDLSNPSRYLCKCPNEFTGDRCONVYIASFY 56

RESULT 12  
US-10-082-747A-108

; Sequence 108, Application US/10082747A  
; Publication No. US20030129688A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ballinger, Marcus D.  
; APPLICANT: Jones, Jennifer T.  
; APPLICANT: Fairbrother, Wayne J.  
; APPLICANT: Sliwkowski, Mark X.  
; APPLICANT: Wells, James A.  
; TITLE OF INVENTION: HERGULIN VARIANTS  
; FILE REFERENCE: 402E-476112US  
; CURRENT APPLICATION NUMBER: US/10/082,747A  
; PRIOR FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: US 09/101,544  
; PRIOR FILING DATE: 1998-07-17  
; PRIOR APPLICATION NUMBER: PCT/US/98/01579  
; PRIOR FILING DATE: 1998-02-10  
; PRIOR APPLICATION NUMBER: US 08/799,054  
; PRIOR FILING DATE: 1997-02-10  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 108  
; LENGTH: 56  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-082-747A-108

Query Match 81.6%; Score 279; DB 4; Length 56;  
Best Local Similarity 88.9%; Pred. No. 3.1e-25;  
Matches 46; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SHLVKCAEKEKTFVNGGECFVMDLSNPSRYLCKCPNEFTGDRCONVYMASFY 54  
Db 3 SHLVKCGEERGFVNGGECFVMDLSNPSRYLCKCPNEFTGDRCONVYIASFY 56

RESULT 13  
US-09-817-647-15

; Sequence 15, Application US/09817647  
; Patent No. US20020082229A1  
; GENERAL INFORMATION:  
; APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao  
; TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/817,647  
; FILING DATE: 26-Mar-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/107,979  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Conley, Delirdre L.  
; REGISTRATION NUMBER: 36,487  
; REFERENCE/DOCKET NUMBER: P1084R1-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/952-9881  
; TELEFAX: 650/952-2066  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 48 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; FEATURE:  
; NAME/KEY: hhrGbeta.egf  
; LOCATION: 1-48  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-817-647-15

Query Match 81.0%; Score 277; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 4.5e-25;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HLVKCAEKEKTFVNGGECFVMDLSNPSRYLCKCPNEFTGDRCONVY 49  
Db 1 HLVKCAEKEKTFVNGGECFVMDLSNPSRYLCKCPNEFTGDRCONVY 48

RESULT 14  
US-09-877-665-15

; Sequence 15, Application US/09877665  
; Patent No. US20020164680A1  
; GENERAL INFORMATION:  
; APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao  
; TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Genentech, Inc.

STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPacIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/877,665  
FILING DATE: 08-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/109,206  
FILING DATE: 30-Jun-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Conley, Delidre L.  
REGISTRATION NUMBER: 36,487  
REFERENCE/DOCKET NUMBER: P1084R1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-2066  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
FEATURE:  
NAME/KEY: bHRGbeta.egf  
LOCATION: 1-48  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-877-665-15

Query Match 81.0%; Score 277; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 4.5e-25;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HLVKAEKEKTCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYV 49  
DB 1 HLVKAEKEKTCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYV 48

RESULT 15  
US-10-136-573A-15  
Sequence 15, Application US/10136573A  
Publication No. US20020161200A1  
GENERAL INFORMATION:  
APPLICANT: Godowski, Paul J.  
APPLICANT: Mark, Melanie Rose  
APPLICANT: Zhang, Dong Xiao  
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related Ligands and  
TITLE OF INVENTION: Uses therefor  
FILE REFERENCE: P1084R1C2  
CURRENT APPLICATION NUMBER: US/10/136,573A  
CURRENT FILING DATE: 2002-04-29  
PRIOR APPLICATION NUMBER: US 09/480,977  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: US 08/899,437  
PRIOR FILING DATE: 1997-07-24  
PRIOR APPLICATION NUMBER: US 60/052,019  
PRIOR FILING DATE: 1997-07-09  
NUMBER OF SEQ ID NOS: 23  
SEQ ID NO 15  
LENGTH: 48  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-136-573A-15

Query Match 81.0%; Score 277; DB 4; Length 48;

Best Local Similarity 100.0%; Pred. No. 4.5e-25;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HLVKAEKEKTCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYV 49  
DB 1 HLVKAEKEKTCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCONYV 48

Search completed: January 26, 2006, 12:54:15  
Job time : 114 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 26, 2006, 12:44:03 ; Search time 32 Seconds

(Without alignments)  
20.643 Million cell updates/sec

Title: US-09-980-672-2

Perfect score: 342  
Sequence: 1 SHLVKAEKKEKTCVNGSEC.....GDRQNTVMASFYKAEELQ 61

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 45467

Minimum DB seq length: 0  
Maximum DB seq length: 61

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88.5	25.9	53	US-11-172-610-5	Sequence 5, Appli
2	87.5	25.6	53	US-11-172-610-7	Sequence 7, Appli
3	77.5	22.7	53	US-11-172-610-2	Sequence 2, Appli
4	73.5	21.5	48	US-11-172-610-6	Sequence 6, Appli
5	71.5	20.9	52	US-11-172-610-4	Sequence 4, Appli
6	70.5	20.6	52	US-11-172-610-3	Sequence 3, Appli
7	70.5	20.6	53	US-11-074-815-1	Sequence 1, Appli
8	70.5	20.6	53	US-11-172-610-1	Sequence 1, Appli
9	66	19.3	50	US-11-172-610-8	Sequence 8, Appli
10	61.5	18.0	45	US-10-055-877-216	Sequence 216, App
11	61.5	18.0	45	US-10-055-877-217	Sequence 217, App
12	61.5	18.0	45	US-10-055-877-218	Sequence 218, App
13	61.5	18.0	45	US-10-055-877-219	Sequence 219, App
14	48.5	14.2	48	US-11-123-896-405	Sequence 405, App
15	46.5	13.7	29	US-10-945-853-8	Sequence 8, Appli
16	46.5	13.6	36	US-10-957-351-17	Sequence 17, Appli
17	46.5	13.6	37	US-10-957-351-72	Sequence 72, Appli
18	44	12.9	18	US-11-128-059-17	Sequence 17, Appli
19	44	12.9	52	US-11-123-896-123	Sequence 123, App
20	44	12.9	52	US-11-123-896-126	Sequence 126, App
21	43.5	12.7	47	US-11-123-896-126	Sequence 126, App
22	42.5	12.4	47	US-11-123-896-162	Sequence 162, App
23	42.5	12.4	47	US-11-123-896-163	Sequence 163, App
24	42	12.3	47	US-11-123-896-429	Sequence 429, App
25	41.5	12.1	49	US-11-123-896-237	Sequence 237, App

26	41	12.0	33	7	US-11-121-301-53	Sequence 53, Appli
27	41	12.0	34	7	US-11-121-301-14	Sequence 14, Appli
28	41	12.0	35	6	US-10-957-351-112	Sequence 112, App
29	41	12.0	47	7	US-11-123-896-456	Sequence 456, App
30	41	12.0	47	7	US-11-019-711-58	Sequence 58, Appli
31	40	11.7	24	7	US-11-128-059-12	Sequence 12, Appli
32	40	11.7	33	7	US-11-113-424-187	Sequence 187, App
33	40	11.7	33	7	US-11-113-424-188	Sequence 188, App
34	40	11.7	33	7	US-11-121-301-51	Sequence 51, Appli
35	40	11.7	33	7	US-11-121-301-52	Sequence 52, Appli
36	40	11.7	35	6	US-10-957-351-26	Sequence 114, App
37	40	11.7	36	6	US-10-957-351-114	Sequence 57, Appli
38	40	11.7	49	7	US-11-019-711-57	Sequence 62, Appli
39	39.5	11.5	37	7	US-11-068-783-62	Sequence 4, Appli
40	39.5	11.5	58	6	US-10-914-391A-4	Sequence 141, App
41	39	11.4	35	6	US-10-957-351-141	Sequence 8, Appli
42	39	11.4	35	7	US-11-121-301-8	Sequence 417, App
43	39	11.4	47	7	US-11-123-896-417	Sequence 357, App
44	38.5	11.3	47	7	US-11-123-896-157	Sequence 399, App
45	38.5	11.3	47	7	US-11-123-896-399	

#### ALIGNMENTS

```

RESULT 1
US-11-172-610-5
; Sequence 5, Application US/11172610
; Publication No. US20060014690A1
; GENERAL INFORMATION:
; APPLICANT: Bishop, Jeffrey S.
; APPLICANT: Loomis, A. Katrina
; APPLICANT: Monticello, Daniel J.
; APPLICANT: Plenkos, Philip T.
; TITLE OF INVENTION: Epidermal Growth Factor Receptor
; FILE REFERENCE: 3530.1002 US2
; CURRENT APPLICATION NUMBER: US/11/172.610
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/643,082
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 60/564,471
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Mouse
US-11-172-610-5

Query Match          25.9%; Score 88.5; DB 7; Length 53;
Best Local Similarity 36.6%; Pred. No. 0.00011;
Matches 15; Conservative 7; Mismatches 16; Indels 3; Gaps 1;

QY      6 CAEKETFCVNGGECFVVKDLSNPSRYLCKCPNEFTGDRQ 46
       6 CPSSYDGVCLNGGVCMHIESLDS---YTCNCVIGSGDRQ 43
Db

RESULT 2
US-11-172-610-7
; Sequence 7, Application US/11172610
; Publication No. US20060014690A1
; GENERAL INFORMATION:
; APPLICANT: Bishop, Jeffrey S.
; APPLICANT: Loomis, A. Katrina
; APPLICANT: Monticello, Daniel J.
; APPLICANT: Plenkos, Philip T.
; TITLE OF INVENTION: Epidermal Growth Factor Receptor
; FILE REFERENCE: 3530.1002 US2
; CURRENT APPLICATION NUMBER: US/11/172.610

```

```

? CURRENT FILING DATE: 2005-06-30
? PRIOR APPLICATION NUMBER: 60/643,082
? PRIOR FILING DATE: 2005-01-11
? PRIOR APPLICATION NUMBER: 60/584,471
? PRIOR FILING DATE: 2004-06-30
? NUMBER OF SEQ ID NOS: 12
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 7
? LENGTH: 53
? TYPE: prt
? ORGANISM: Rat
? JS-11-172-610-7

```

Query Match	25.6%	Score	87.5	DB	7	Length	53
Best Local Similarity	35.7%	Pred.	No.	0.00014			
Matches	15	Conservative	8	Mismatches	16	Indels	3
						Gaps	1

```

QY      6 CAEKETFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCON 47
        |  ::|||  |  ::  |||  |  ::|||  :
Db      6 CPSPYDGYCLNGGVCMYVESV--DRVVCNCVIGYIGERQCH 44

```

```

RESULT 3
US-11-172-610-2
; Sequence 2, Application US/11172610
; Publication No. US20060014690A1
; GENERAL INFORMATION:
; APPLICANT: Bishop, Jeffrey S.
; APPLICANT: Loomis, A. Katrina
; APPLICANT: Monticello, Daniel J.
; APPLICANT: Pienkos, Philip T.
; TITLE OF INVENTION: Epidermal Growth Factor Receptor
; TITLE OF INVENTION: Antagonists and Methods of Use
; FILE REFERENCE: 3530.1002 US2
; CURRENT APPLICATION NUMBER: US/11/172,610
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/643,082
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 60/584,471
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 53
; TYPE: prt
; ORGANISM: pig
US-11-172-610-2

```

Query Match	22.7%	Score 77.5;	DB 7;	Length 53;
Best Local Similarity	27.9%	Pred. No. 0.0024		
Matches 12; Conservative	11;	Mismatches 17;	Indels 3;	Gaps 1

```

RESULT 4
US-11-172-610-6
; Sequence 6, Application US/11172610
; Publication No. US20060014690A1
; GENERAL INFORMATION:
; APPLICANT: Biotrop, Jeffrey S.
; APPLICANT: Loomis, A. Katrina
; APPLICANT: Monticello, Daniel J.
; APPLICANT: Plentos, Philip T.
; TITLE OF INVENTION: Epidermal Growth Factor Receptor
; TITLE OF INVENTION: Antagonists and Methods of Use
; FILE REFERENCE: 3530.1002 US2
; CURRENT APPLICATION NUMBER: US/11/172,610
; CURRENT FILING DATE: 2005-06-30
; PRIORITY APPLICATION NUMBER: 60/643,082
; PRIOR FILING DATE: 2005-01-11

```

```

? PRIOR APPLICATION NUMBER: 60/584,477
? PRIOR FILING DATE: 2004-06-30
? NUMBER OF SEQ ID NOS: 12
? SOFTWARE: FASTSEQ for Windows Version
? SEQ ID NO: 6
? LENGTH: 48
? TYPE: prt
? ORGANISM: Horae
? JS-11-172-610-6

```

Query Match	21.5%;	Score	73.5;	DB	7;	Length	48;
Best Local Similarity	25.6%;	Pred. No.	0.0068;				
Matches	11;	Conservative	13;	Mismatches	16;	Indels	3;
						Gaps	1;

```
QY      5 KCAEKEKTFVANGGECFVWKDLSNPSRYLCKPCNFEFTGRCON 47
Db      5 ECSQSYDGYCLHGKCVYLQVDT--HACNCVVGIVGERCOH 44
```

```

RESULT 5
US-11-172-610-4
, Sequence 4, Application US/11172610
, Publication No. US20060014690A1
, GENERAL INFORMATION:
, APPLICANT: Bishop, Jeffrey S.
, APPLICANT: Loomis, A. Katrina
, APPLICANT: Monticello, Daniel J.
, APPLICANT: Pienkos, Philip T.
, TITLE OF INVENTION: Epidermal Growth Factor Receptor
, TITLE OF INVENTION: Antagonists and Methods of Use
, FILE REFERENCE: 3530.1002 US2
, CURRENT APPLICATION NUMBER: US/11/172,610
, PRIORITY FILING DATE: 2005-06-30
, PRIOR APPLICATION NUMBER: 60/643,082
, PRIOR FILING DATE: 2005-01-11
, PRIOR APPLICATION NUMBER: 60/584,471
, PRIOR FILING DATE: 2004-06-30
, NUMBER OF SEQ ID NOS: 12
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO 4
, LENGTH: 52
, TYPE: prt
, ORGANISM: Dog
US-11-172-610-4

```

Query Match 20.9%; Score 71.5; DB 7; Length 52;  
 Best Local Similarity 27.9%; Pred. No. 0.013;  
 Matches 12; Conservative 9; Mismatches 19; Indels 3; Gaps 1;

```

RESULT 6
US-11-172-610-3
; Sequence 3, Application US/11/172610
; Publication No. US20060014650A1
; GENERAL INFORMATION:
; APPLICANT: Bishop, Jeffrey S.
; APPLICANT: Loomis, A. Katrina
; APPLICANT: Monticello, Daniel J.
; APPLICANT: Plentos, Philip T.
; TITLE OF INVENTION: Epidermal Growth Factor Receptor
; TITLE OF INVENTION: Antagonists and Methods of Use
; FILE REFERENCE: 3530.1002 US2
; CURRENT APPLICATION NUMBER: US/11/172,610
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/643,082
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 60/584,471
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 12

```



US-11-172-610-

APPLICANT: Shimkets, Richard

APPLICANT: Shimkets, Richard

```

; APPLICANT: Verneet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; PRIOR APPLICATION NUMBER: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 216
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EGF domain
; OTHER INFORMATION: consensus sequence
US-10-055-877-216

Query Match      18.0%; Score 61.5; DB 6; Length 45;
Best Local Similarity 38.5%; Pred. No. 0.19;
Matches 15; Conservative 2; Mismatches 15; Indels 7; Gaps 2;

QY      14  CVNGGECFMVKDLS--NPSRYLCKCPN-----EFTGDRG 45
Db      7  CSNGGTCVNTPGGSSDNFGYTCPCPRDYLYLSTGKRC 45

RESULT 11
US-10-055-877-217
; Sequence 217, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tcherenev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zernhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
```

```

; APPLICANT: Burgess, Catherine
; APPLICANT: Bisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Verneet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; PRIOR APPLICATION NUMBER: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 217
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EGF domain
; OTHER INFORMATION: consensus sequence
US-10-055-877-217

Query Match      18.0%; Score 61.5; DB 6; Length 45;
Best Local Similarity 38.5%; Pred. No. 0.19;
Matches 15; Conservative 2; Mismatches 15; Indels 7; Gaps 2;

QY      14  CVNGGECFMVKDLS--NPSRYLCKCPN-----EFTGDRG 45
Db      7  CSNGGTCVNTPGGSSDNFGYTCPCPRDYLYLSTGKRC 45

RESULT 12
US-10-055-877-218
; Sequence 218, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tcherenev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
```

APPLICANT: Kekuda, Rameesh  
APPLICANT: Guo, Xiaojia  
APPLICANT: Zethusen, Bryan  
APPLICANT: Andrew, David  
APPLICANT: Mezes, Peter  
APPLICANT: Patturajan, Meera  
APPLICANT: Burgess, Catherine  
APPLICANT: Eisen, Andrew  
APPLICANT: Wolenc, Adam  
APPLICANT: Baumgartner, Jason  
APPLICANT: Shinkets, Richard  
APPLICANT: Gusev, Vladimir  
APPLICANT: Vernet, Corine  
APPLICANT: Taupier Jr., Raymond  
APPLICANT: Pena, Carol  
APPLICANT: Shenoy, Suresh  
APPLICANT: Li, Li  
APPLICANT: Casman, Stracie  
APPLICANT: Boldog, Ferenc  
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby  
FILE REFERENCE: 21402-251  
CURRENT APPLICATION NUMBER: US/10/055,877  
CURRENT FILING DATE: 2002-01-22  
PRIOR APPLICATION NUMBER: 60/262,892  
PRIOR FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: 60/263,598  
PRIOR FILING DATE: 2001-01-23  
PRIOR APPLICATION NUMBER: 60/263,799  
PRIOR FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: 60/264,117  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 60/264,139  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 60/264,478  
PRIOR FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 60/263,351  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: 60/272,870  
PRIOR FILING DATE: 2001-03-02  
PRIOR APPLICATION NUMBER: 60/275,990  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/275,927  
PRIOR FILING DATE: 2001-03-14  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 512  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 218  
LENGTH: 45  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: EGF domain  
US-10-055-877-218

Query Match 18.0%; Score 61.5; DB 6; Length 45;  
Best Local Similarity 38.5%; Pred. NO. 0.19;  
Matches 15; Conservative 2; Mismatches 15; Indels 7; Gaps 2;

QY 14 CVMGCECMVWDL-S-NPSRYLCKCPN-----EFTGDRG 45  
DB 7 CSNGTCVNTPGSSDNFGYTCBCPPGDYLYSTGRKC 45

RESULT 13  
US-10-055-877-219  
Sequence 219, Application US/10055877  
Publication No. US20050288241A1  
GENERAL INFORMATION:  
APPLICANT: Decristofaro, Marc  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Miller, Charles  
APPLICANT: Tchiernev, Velizar

APPLICANT: Zhong, Mei  
APPLICANT: Anderson, David  
APPLICANT: Baillinger, Robert  
APPLICANT: Gerlach, Valerie  
APPLICANT: Spytek, Kimberly  
APPLICANT: Ratelli, Luca  
APPLICANT: Kekuda, Rameesh  
APPLICANT: Guo, Xiaojia  
APPLICANT: Zethusen, Bryan  
APPLICANT: Andrew, David  
APPLICANT: Mezes, Peter  
APPLICANT: Patturajan, Meera  
APPLICANT: Burgess, Catherine  
APPLICANT: Eisen, Andrew  
APPLICANT: Wolenc, Adam  
APPLICANT: Baumgartner, Jason  
APPLICANT: Shinkets, Richard  
APPLICANT: Gusev, Vladimir  
APPLICANT: Vernet, Corine  
APPLICANT: Taupier Jr., Raymond  
APPLICANT: Pena, Carol  
APPLICANT: Shenoy, Suresh  
APPLICANT: Li, Li  
APPLICANT: Casman, Stracie  
APPLICANT: Boldog, Ferenc  
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby  
FILE REFERENCE: 21402-251  
CURRENT APPLICATION NUMBER: US/10/055,877  
CURRENT FILING DATE: 2002-01-22  
PRIOR APPLICATION NUMBER: 60/262,892  
PRIOR FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: 60/263,598  
PRIOR FILING DATE: 2001-01-23  
PRIOR APPLICATION NUMBER: 60/263,799  
PRIOR FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: 60/264,117  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 60/264,139  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 60/264,478  
PRIOR FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 60/263,351  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: 60/272,870  
PRIOR FILING DATE: 2001-03-02  
PRIOR APPLICATION NUMBER: 60/275,990  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/275,927  
PRIOR FILING DATE: 2001-03-14  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 512  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 219  
LENGTH: 45  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: EGF domain  
US-10-055-877-219

Query Match 18.0%; Score 61.5; DB 6; Length 45;  
Best Local Similarity 38.5%; Pred. NO. 0.19;  
Matches 15; Conservative 2; Mismatches 15; Indels 7; Gaps 2;

QY 14 CVMGCECMVWDL-S-NPSRYLCKCPN-----EFTGDRG 45  
DB 7 CSNGTCVNTPGSSDNFGYTCBCPPGDYLYSTGRKC 45

RESULT 14  
US-11-123-896-405  
Sequence 405, Application US/11123896

```
/ Publication No. US20050273881A1
/ GENERAL INFORMATION:
/ APPLICANT: Simmons, Carl R.
/ APPLICANT: Navarro Acevedo, Pedro A.
/ APPLICANT: Harvell, Leslie
/ APPLICANT: Cahoon, Rebecca
/ APPLICANT: McCutchen, Billy Fred
/ APPLICANT: Lu, Albert
/ APPLICANT: Hermann, Rafael
/ APPLICANT: Wong, James
/ TITLE OF INVENTION: Defensin Polynucleotides and Methods of
/ FILE REFERENCE: 35718/246703
/ CURRENT APPLICATION NUMBER: US/11/123,896
/ PRIOR FILING DATE: 2005-05-06
/ PRIOR APPLICATION NUMBER: 60/300,152
/ PRIOR FILING DATE: 2001-06-22
/ PRIOR APPLICATION NUMBER: 60/300,241
/ PRIOR FILING DATE: 2001-06-22
/ NUMBER OF SEQ ID NOS: 469
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 405
/ LENGTH: 48
/ TYPE: PRT
/ ORGANISM: Rictinus communis
US-11-123-896-405
```

```
Query Match      14.2%; Score 48.5; DB 7; Length 48;
Best Local Similarity 23.9%; Pred. No. 8.1;
Matches 11; Conservative 6; Mismatches 16; Indels 13; Gaps 2;
```

```
Qy      6 CAEKEKTF---CVNGGECFMYKDLSPSRYLCKCPNEFTGDRCONY 48
Db      3 CESKSHHFHGPCLRDHNCALV-----CRTEGNFSGGRCKRGF 38
```

```
RESULT 15
US-10-945-853-8
/ Sequence 8, Application US/10945853
/ Publication No. US20050255117A1
/ GENERAL INFORMATION:
/ APPLICANT: Biogen, Inc.
/ APPLICANT: Sanicola-Nadel, Michele
/ APPLICANT: Adkins, Heather
/ APPLICANT: Miklasz, Steven Donald
/ APPLICANT: Rayhorn, Paul
/ APPLICANT: Schiffer, Susan Gail
/ APPLICANT: Williams, Kevin
/ TITLE OF INVENTION: Crip-to-Specific Antibodies
/ FILE REFERENCE: BGN117CPCCN
/ CURRENT APPLICATION NUMBER: US/10/945,853
/ CURRENT FILING DATE: 2004-09-20
/ PRIOR APPLICATION NUMBER: PCT/US02/31462
/ PRIOR FILING DATE: 2002-10-01
/ PRIOR APPLICATION NUMBER: PCT/US02/11950
/ PRIOR FILING DATE: 2002-04-17
/ PRIOR APPLICATION NUMBER: 60/286,782
/ PRIOR FILING DATE: 2001-04-26
/ PRIOR APPLICATION NUMBER: 60/293,020
/ PRIOR FILING DATE: 2001-05-17
/ PRIOR APPLICATION NUMBER: 60/301,091
/ PRIOR FILING DATE: 2001-06-26
/ PRIOR APPLICATION NUMBER: 60/367,002
/ PRIOR FILING DATE: 2002-03-22
/ NUMBER OF SEQ ID NOS: 9
/ SEQ ID NO 8
/ LENGTH: 29
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: Mod_res
/ LOCATION: 1
/ OTHER INFORMATION: N-terminal acetylation
```

US-10-945-853-8

```
Query Match      13.7%; Score 47; DB 6; Length 29;
Best Local Similarity 28.6%; Pred. No. 7.6;
Matches 10; Conservative 4; Mismatches 13; Indels 8; Gaps 1;
```

```
Qy      15 VNGGECFMYKDLSPSRYLCKCPNEFTGDRCONYV 49
Db      1 LNEGTCLGS-----FCACPPSYGRNCEHDV 27
```

Search completed: January 26, 2006, 12:54:58  
Job time : 33 secs